

FIG. 2A

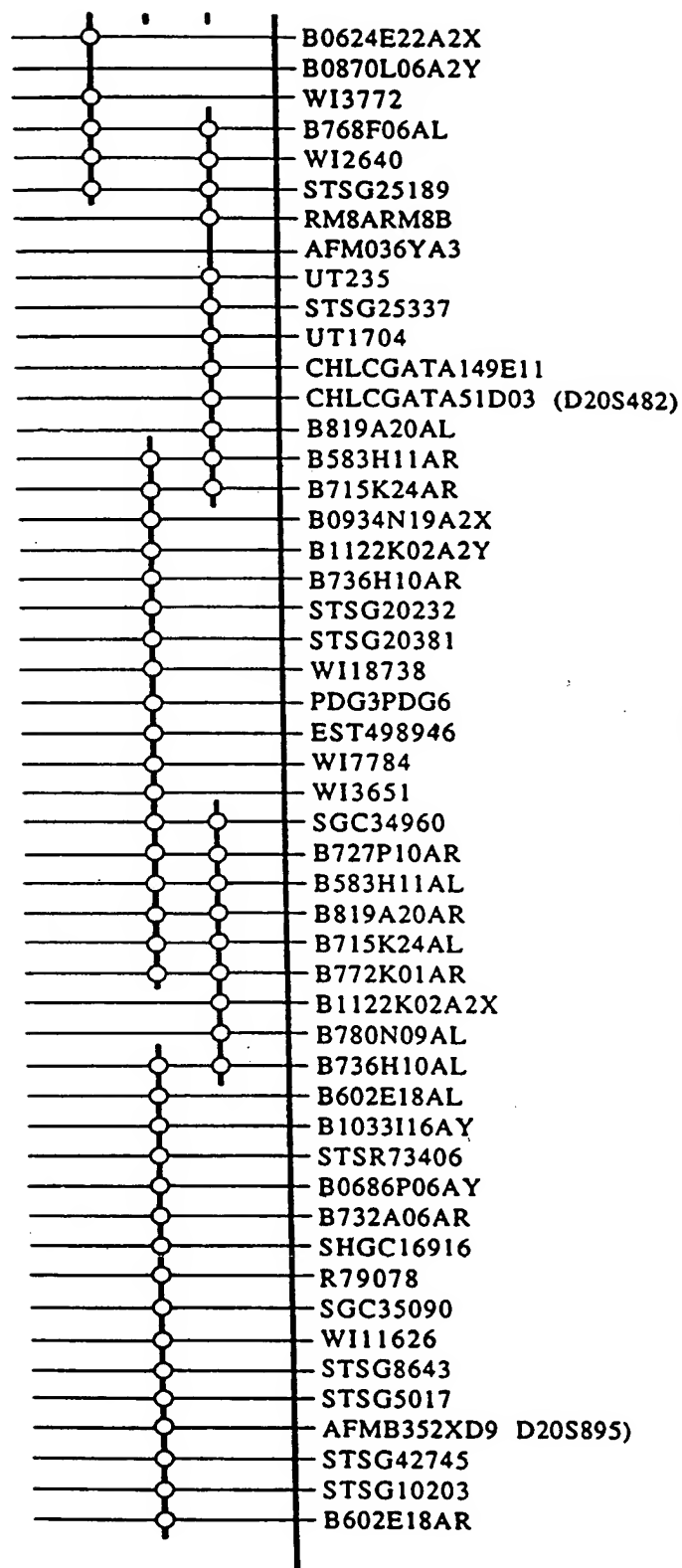


FIG. 2B

10 30 50
 ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTACTACTGCTG
 MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeu

70 90 110
 CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGCCAGTC
 LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnProVal

130 150 170
 ACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTC
 ThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProVal

190 210 230
 TCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAG
 SerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuLeuGlu

250 270 290
 CTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGAT
 LeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyProAsp

310 330 350
 GGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTA
 GlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgVal

370 390 410
 AGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATC
 ArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIle

430 450 470
 ACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCGGGGCTCCAAGGAC
 ThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAsp

490 510 530
 TTCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGC
 PheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGly

550 570 590

FIG. 3A

CACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGG
HisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArg

610 630 650

GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCAC
GlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHis

670 690 710

ACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTC
ThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluVal

730 750 770

GCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTG
AlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeu

790 810 830

GAGGTGTGGACCGAGCGGGACCGCAGCCGCTCACGCAGGACGCCAACGCCACGCTCTGG
GluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrp

850 870 890

GCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTG
AlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeu

910 930 950

CTCACGGGCCCGCCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGC
LeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCys

970 990 1010

CGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCA
ArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAla

1030 1050 1070

GCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGC
AlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCys

1090 1110 1130

TGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCG
CysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisPro

FIG. 3B

1150 1170 1190
TTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGG
PheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGly

1210 1230 1250
GGCGGCGCTTGCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGC
GlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCys

1270 1290 1310
GGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGC
GlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArg

1330 1350 1370
GACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGG
AspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGly

1390 1410 1430
GACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGT
AspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGly

1450 1470 1490
GACTGTGACCTCCCTGAGTTTTCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTAC
AspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyr

1510 1530 1550
CTACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCC
LeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysPro

1570 1590 1610
ACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCCTGATGGCCAGGAAGTGACTTGTCGG
ThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProAspGlyGlnGluValThrCysArg

1630 1650 1670
GGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCA
GlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluPro

1690 1710 1730

FIG. 3C

GGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTC
 GlyThrGlnCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPhe

1750 1770 1790
 CAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGCAATAGCAACCAT
 GlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHis

1810 1830 1850
 AACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGC
 AsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGly

1870 1890 1910
 AGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATGCTC
 SerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMetLeu

1930 1950 1970
 CTCAGCGTCCCTGCTGCCTCTGCTCCCAGGGCCGGCCTGGCCTGGTGTGCTACCGACTC
 LeuSerThrLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArgLeu

1990 2010 2030
 CCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGGC
 ProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSerGly

2050 2070 2090
 CCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTCACCCCATGGAGTTGGGC
 ProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeuGly

2110 2130 2150
 CCCACAGCCACTGGACAGCCCTGGCCCCCTGGACCCTGAGAACTCTCATGAGCCCAGCAGC
 ProThrAlaThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSerSer

2170 2190 2210
 CACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAGATG
 HisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGlnValGlnMet

2230 2250 2270
 CCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGG
 ProArgSerCysLeuTrpEnd

FIG. 3D

2290 2310 2330
CCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAATCACCGGACC

2350 2370 2390
TCCAGCACCTGCAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACT

2410 2430 2450
CCAGGAACCCAGAGCCACATTAGAAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCACACT

2470 2490 2510
CTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCTGACCTCCCTC

2530 2550 2570
ACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAGGGCTCTGTCCTGGGAGTCTGGTG

2590 2610 2630
TGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGA

2650 2670 2690
AGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCTGCAGCCTGGCTG

2710 2730 2750
GCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCTGTCTT

2770 2790 2810
CTCCCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCCAGTGCTACACCTGAGGTTCTGG

2830 2850 2870
AGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTCTGGGGGGACAGAGGGAACCA

2890 2910 2930
TTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGCGTGGTG

FIG. 3E

2950 2970 2990
GCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGAGGCCAG

3010 3030 3050
GAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA

3070 3090 3110
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAG

3130 3150 3170
GATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCACTCCAGC

3190 3210 3230
CTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATATTAAAAAA

3250 3270
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 3F

10	30	50
ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTACTACTGCTG		
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeu		
70	90	110
CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGCCAGTC		
LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnProVal		
130	150	170
ACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTC		
ThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProVal		
190	210	230
TCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAG		
SerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuLeuGlu		
250	270	290
CTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGAT		
LeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHis <u>Tyr</u> GlyProAsp		
310	330	350
GGGCAGCCAGTGGTGGCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTA		
GlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgVal		
370	390	410
AGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATC		
ArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIle		
430	450	470
ACCGTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGAC		
ThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAsp		
490	510	530
TTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGC		
PheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGly <u>Thr</u> CysGly		
550	570	590

FIG. 4A

CACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGG
HisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArg

610 630 650
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAACGTACATTGTGGCAGACCAC
GlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHis

670 690 710
ACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTC
ThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluVal

730 750 770
GCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTG
AlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeu

790 810 830
GAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGG
GluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrp

850 870 890
GCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTG
AlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeu

910 930 950
CTCACGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGC
LeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCys

970 990 1010
CGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCA
ArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAla

1030 1050 1070
GCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGC
AlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCys

1090 1110 1130
TGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCG
CysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisPro

FIG. 4B

1150 1170 1190
TTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGG
PheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGly

1210 1230 1250
GGCGGCGCTTGCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGC
GlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCys

1270 1290 1310
GGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGC
GlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArg

1330 1350 1370
GACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCCACGGG
AspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGly

1390 1410 1430
GACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGT
AspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGly

1450 1470 1490
GACTGTGACCTCCCTGAGTTTGGCACGGGCACCTCCTCCCACTGTCCCCAGACGTTTAC
AspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyr

1510 1530 1550
CTACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCC
LeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysPro

1570 1590 1610
ACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCC
ThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAla

1630 1650 1670
TGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAG
CysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGlu

1690 1710 1730

FIG. 4C

GGCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGT
 GlyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGly

1750 1770 1790
 GGAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGAAGCTTACCGTTACCTAGAT
 GlyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAsp

1810 1830 1850
 GGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTT
 GlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeu

1870 1890 1910
 GGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTTTGAATAGCAAC
 GlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysAsnSerAsn

1930 1950 1970
 CATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGT
 HisAsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGly

1990 2010 2030
 GGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATG
 GlySerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMet

2050 2070 2090
 CTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCCGGCCTGGCCTGGTGTGCTACCGA
 LeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArg

2110 2130 2150
 CTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCACT
 LeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSer

2170 2190 2210
 GGCCCCAAAGATGGCCCCACACAGGGACCACCCCTGGGCGGCGTTACCCCATGGAGTTG
 GlyProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeu

2230 2250 2270
 GGCCCCACAGCCACTGGACAGCCCTGGCCCCTGGACCCTGAGAACTCTCATGAGCCCAGC
 GlyProThrAlaThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSer

FIG. 4D

2290 2310 2330
AGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAG
SerHisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGlnValGln

2350 2370 2390
ATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGG
MetProArgSerCysLeuTrpEnd

2410 2430 2450
TGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAATCACCGG

2470 2490 2510
ACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCC

2530 2550 2570
ACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCAC

2590 2610 2630
ACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCCTGACCTCC

2650 2670 2690
CTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCCAAAAGGGCTCTGTCCTGGGAGTCTG

2710 2730 2750
GTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTGGCC

2770 2790 2810
AGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCCTGCAGCCTGG

2830 2850 2870
CTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCTGT

2890 2910 2930
CTTCTCCCCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCCAGTGCTACACCTGAGGTTT

FIG. 4E

2950 2970 2990
TGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTCGGGGGGACAGAGGGAA

3010 3030 3050
CCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGCGTG

3070 3090 3110
GTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGAGGC

3130 3150 3170
CAGGAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTA

3190 3210 3230
AAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAG

3250 3270 3290
GAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCACTCC

3310 3330 3350
AGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATATTAAAA

3370 3390
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 4F

10 30 50
 ATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTG
 MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuLeuLeu

70 90 110
 CTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGTGAGGACGCGGGCGGGGTCCCC
 LeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyGluAspAlaGlyGlyValPro

130 150 170
 CTCACCCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGGCAGCCAGTCACCCCGCAC
 LeuThrLeuCysSerValPheThrProGlyHisIleProGlyGlnProValThrProHis

190 210 230
 TGGGTCTTGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGCCA
 TrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluProValSerLysPro

250 270 290
 GACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAG
 AspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuLeuGluLeuGluLys

310 330 350
 AACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCA
 AsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyProAspGlyGlnPro

370 390 410
 GTGGTGCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTC
 ValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyArgValArgGlyPhe

430 450 470
 CCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCACCTCAGC
 ProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIleThrLeuSer

490 510 530
 AGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACC
 ArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThr

550 570 590

FIG. 5A

CACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAAGGAACCTGTGGCCACAGGGAT
HisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyHisArgAsp

610

630

650

CCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGGGCAGGCGA
ProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArgGlyArgArg

670

690

710

GAAGCGCGCAGGACCCGGAAGTACCTGGAACGTACATTGTGGCAGACCACACCCTGTTC
GluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHisThrLeuPhe

730

750

770

TTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTAC
LeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValAlaAsnTyr

790

810

830

GTGGACCAGCTTCTCAGGACTCTGGACATTTCAGGTGGCGCTGACCGCCTGGAGGTGTGG
ValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeuGluValTrp

850

870

890

ACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCCTG
ThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrpAlaPheLeu

910

930

950

CAGTGGCGCCGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGGGC
GlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeuLeuThrGly

970

990

1010

CGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCCGCGCCGAG
ArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCysArgAlaGlu

1030

1050

1070

AGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCAGCCACCATG
SerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAlaAlaThrMet

1090

1110

1130

GCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGGAG
AlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCysCysValGlu

FIG. 5B

1150 1170 1190
GCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGC
AlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisProPheProArg

1210 1230 1250
GTGTTTCAGCGCCTGCAGCCGCCGAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCT
ValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGlyGlyGlyAla

1270 1290 1310
TGCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGCGGGAACGGC
CysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCysGlyAsnGly

1330 1350 1370
TTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGCGACCTCTGC
PheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArgAspLeuCys

1390 1410 1430
TGCTTTGCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGGGACTGCTGC
CysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGlyAspCysCys

1450 1470 1490
GTGCGCTGCGCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGAC
ValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGlyAspCysAsp

1510 1530 1550
CTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTACCTACTGGAC
LeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyrLeuLeuAsp

1570 1590 1610
GGCTCACCCCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCACGCTGGAG
GlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysProThrLeuGlu

1630 1650 1670
CAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTTCCAG
GlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAlaCysPheGln

1690 1710 1730

FIG. 5C

GTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTC
ValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPhe

1750

1770

1790

CTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCC
LeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysPro

1810

1830

1850

AGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAA
SerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAspGlyGlnGlu

1870

1890

1910

GTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGC
ValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGly

1930

1950

1970

CTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGG
LeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnSerArgArgCysArg

1990

2010

2030

AAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGC
LysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisGlyValCys

2050

2070

2090

AATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCA
AsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProPheCysAspLysPro

2110

2130

2150

GGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTG
GlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnHisAspThrPheLeu

2170

2190

2210

CTGGCCATGCTCCTCAGCGTCTCTGCTGCCAGGGGCCGGCCTGGCCTGGTGT
LeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCys

2230

2250

2270

TGCTACCGACTCCCAGGAGCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCCT
CysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgArgAspPro

FIG. 5D

2290 2310 2330
GCGTGCAGTGGCCCCAAAGATGGCCCCACACAGGGACCACCCCTGGGCGGCGTTCACCCC
AlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGlyValHisPro

2350 2370 2390
ATGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGCCCCAGGGTCTCCTGCT
MetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAlaProGlySerProAla

2410 2430 2450
GACCATATTCAACATTTACCCTCCACCATTCTCTCCAGACCCTGAGAACTCTCATGAG
AspHisIleHisAsnIleTyrProProProPheLeuProAspProGluAsnSerHisGlu

2470 2490 2510
CCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAA
ProSerSerHisProGluLysProLeuProAlaValSerProAspProGlnAlaAspGln

2530 2550 2570
GTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAA
ValGlnMetProArgSerCysLeuTrpEnd

2590 2610 2630
GACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCAGAGCCAGTGAAT

2650 2670 2690
CACCGGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGTGGAGCTTCGAC

2710 2730 2750
CCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCCTGAGGGCTGGAGAACTGCT

2770 2790 2810
GGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCCTG

2830 2850 2870
ACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCCAAAAGGGCTCTGTCTCTGGG

FIG. 5E

2890 2910 2930
AGTCTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTG

2950 2970 2990
CTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCACACTCCCCTGSA

3010 3030 3050
GCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCA

3070 3090 3110
CCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCCAATCCCAGTGCTACACCTG

3130 3150 3170
AGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATCTGTGTGTGTGCGGGGGGACAG

3190 3210 3230
AGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGTTGGCTATA

3250 3270 3290
GGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCYGGGGTAGGAGGATCACC

3310 3330 3350
AGAGGCCAGSAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAAAAA

3370 3390 3410
ATTTTAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTG

3430 3450 3470
AAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTG

3490 3510 3530
CACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATA

3550 3570

FIG. 5F

TTAA

FIG. 5G

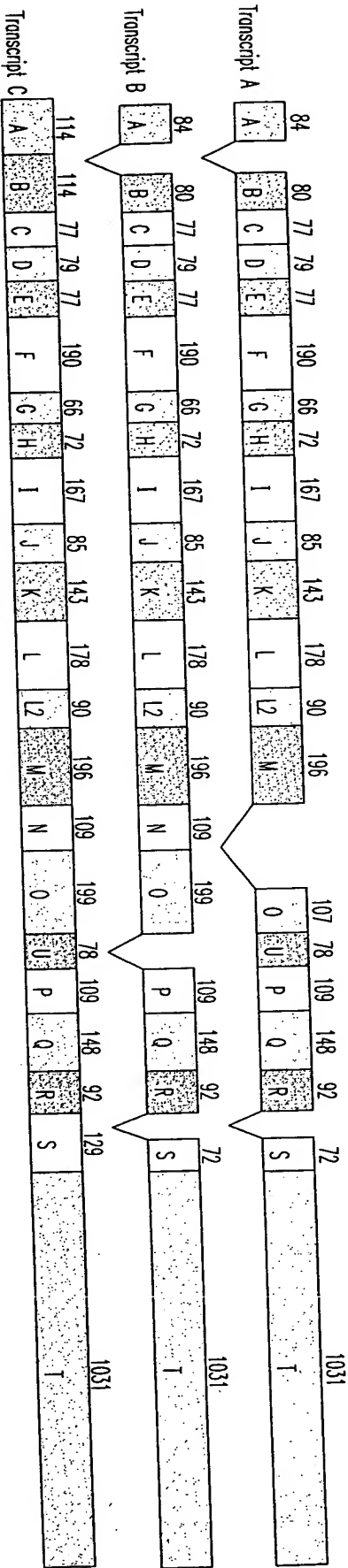


FIG. 6

>Gene216_A
ATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAG

>Gene216_B
GACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGGTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTCCGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCCTGGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCCTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCACCCGTTTCCGCGCTGTTTCAGCGCCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCCGACCCCGGACTCCCGGTGCCGCCGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGCCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAACTGCTCGCTGCGCCCGGGGGGCCAGTGCGCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTG

>Gene216_O

FIG. 7A

ATGGCCAGGAAGTGACTTGTCTGGGGAGCCTTGGCACTCCCCAGTGCCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAG
CCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_U_Alt
GTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGG

>Gene216_P
GTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCGCTGGCCTGGTGTTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S
ACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAACCTTGAAGTGCAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCCGAGTGGAGCTTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCCCTGACCTCCCTCACC
AGTGGAGGCTGGGTAGTGTCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACT
CCCCTGGAGCCTGGCTGGCCTCTGCAAACAAACATAATTTGGGGACCTTCCTTCTGTTTCTTCCCACCCTGTCTTCTC
CCCTAGGTGGTTCTGAGCCCCCACCCTCAATCCAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTCTGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAAGCTATGGTGG
CACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAGACATATTA

FIG. 7B

>Gene216_A
ATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAG

>Gene216_B
GACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGSCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCCTGGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAACTTGAACCACACCAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAAGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCAAGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCCGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGGGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGGCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTCTGCTGCGTGGCGCCGGGGGGCCAGTGCGCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTGTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTG

FIG. 8A

>Gene216_N_Alt
GCTCCCACCCAGCTCCCAGGCCTGTTTCCAGGTGGTGAACCTCGCGGAGATGCTCATGGAACTGCGGCCAGGACAGC
GAGGGCCACTTCCTGCCCTGTGCAGGGAG

>Gene216_O_Alt
GGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTA
CCGTTTACCTAGATGGCCAGGAAGTGAAGTGTGCGGGAGCCTTGGCACTCCCCAGTGGCAGCTGGACCTGCTTGGCCTG
GGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_P
GTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCCTGGCCTGGTGTTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGGCCACACAGGGACCACCCCTGGGCGGCGTTACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S
ACCCTGAGAAGTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAAGTGAAGTGCAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCCTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCCCTGACCTCCCTCACC
AGTGGAGGCTGGGTAGTGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTTCGACTGAGTCCACACT
CCCCCTGGAGCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCTGTTTCTTCCCACCCTGTCTTCTC
CCCTAGGTGGTTCCTGAGCCCCACCCCAATCCCAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTGCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAAGCTATGGTGG
CACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAGACATATTA

FIG. 8B

>Gene216_A_Alt
ATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGG
CGCCGGGGTGCTTCAAGGTGAGGACGCGGGCGGG

>Gene216_B_Alt
GTCCCCCTCACCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTTGATGG
ACAACCTTGGCGCACCGTCAGCCTGGAGGAGCCG

>Gene216_C
GTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCA

>Gene216_D
CAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGGCAGCCAGTGGTGTGGCCCCCAACCACAG

>Gene216_E
GATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAG

>Gene216_F
TGGCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCC
ACGAGATCTTTCGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATG
ACCAGCCTTCTGTGGTCCCCAGAGCAGG

>Gene216_G
GGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTG

>Gene216_H
TTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAG

>Gene216_I
CTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCA
GGACGCCAACGCCACGCTCTGGGCCTTCTTGCACTGGCGCCGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGC
TGCTCAC

>Gene216_J
GGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTGGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGA
GCACG

>Gene216_K
GACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCC
CGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGG

>Gene216_L1
GCA~~C~~CCGTTTCCGCGCGTGTTACGCGCCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCC
TCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGCGGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGT
GACTGCGGCCCTGGCCAG

>Gene216_L2
GAGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTGTGCTGCGTGGCGCCGGGGGGCCAGTGGCGCCACGGGGACTGCTGCGT
GCGCTGCCTG

>Gene216_M
CTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTG:ACGGGCACCTCCTCCCA
CTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGATGGCGCATGTCCCA
CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTG

FIG. 9A

>Gene216_N_Alt
GCTCCACCCAGCTCCCGAGGCTGTTTCCAGGTGGTGAAGTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGC
GAGGGCCACTTCTGCCCTGTGCAGGGAG

>Gene216_O_Alt
GGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTA
CCGTTCACTTAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTG
GGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATG

>Gene216_U_Alt
GTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGG

>Gene216_P
GTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAG
CATGGACAGTGGCCCTGTGCAGGCTGAAA

>Gene216_Q
ACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCGGCGCTGGCCTGGTGTGTC
TACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGG

>Gene216_R
CCCCAAAGATGGCCACACAGGGACCACCCCCTGGGCGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGC
CCTGGCCCCCTGG

>Gene216_S_Alt
CCCCAGGGTCTCCTGCTGACCATATTCACAACATTTACCCTCCACCATTTCTCCAGACCCTGAGAACTCTCATGAGCCC
AGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAG

>Gene216_T
CAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAAATGAACAGATTTAAAGACAGGTGGCCA
CTGACAGCCACTCCAGGAAGTTGAACTGCAGGGGCGAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGG
AAGTTTCTTCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTGAGGGCTGGAGA
ACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCCTGACCTCCCTCAC
AGTGGAGGCTGGGTAGTGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCAC
GGACCCAGCTCTGTGAGGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACT
CCCCTGGAGCCTGGCTGGCCTCTGCAACAAACATAATTTGGGGACCTTCCTTCTGTTTCTTCCACCCTGTCTTCTC
CCCTAGGTGGTTCTCTGAGCCCCCACCCTCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTC
CCCCATTCTGTGTGTGTGCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACATGT
TGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCTGGGGTAGGAGGATCACCAGAGGCCAGGAG
GTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTA
CCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGG
CACCCTGCACCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAATAAATTTTAAAAAGACATATTA

FIG. 9B

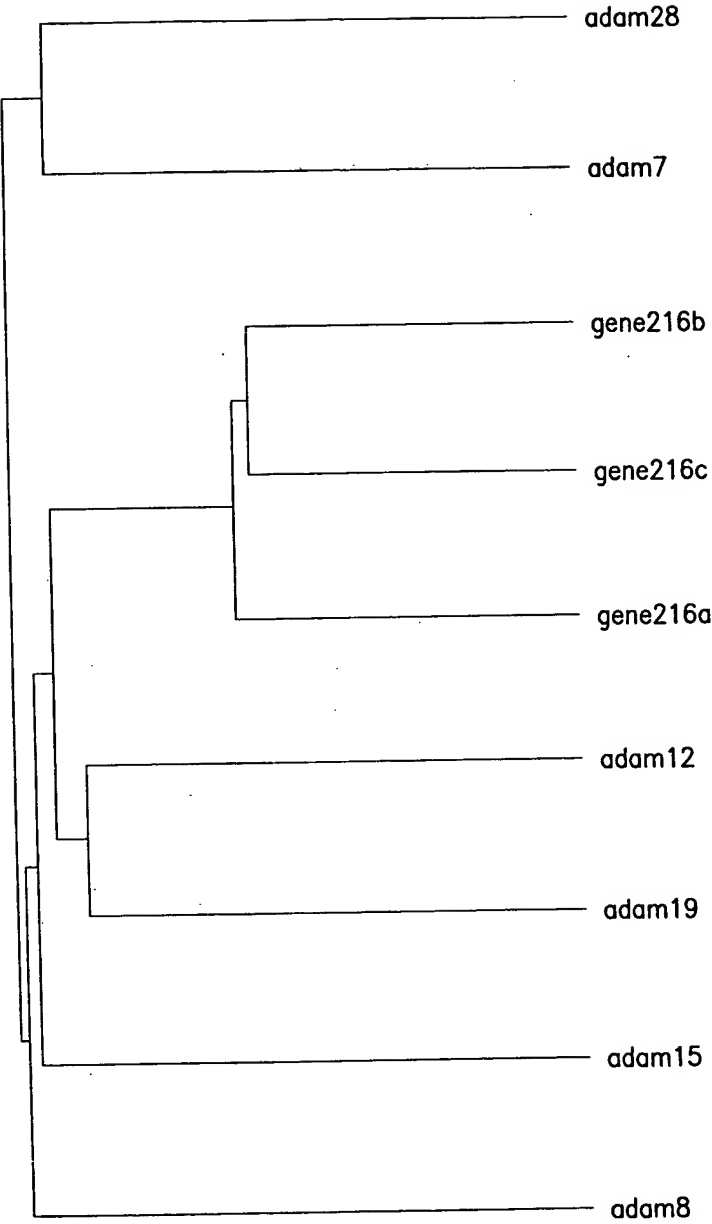


FIG. 10

		Signal sequence →						
		1				50		
adam28		M-----	-----	-----	~LQG	LLPVSLLLSV	AVSAIKELPG	
adam7		-----	-----	-----	-----	-----	-----	
gene216b		MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQ.....G		
gene216c		MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQGEDAGGVP	LTLCSVFTPG		
gene216a		MGWRPRRARG	TPLLLLLLLL	LLWPVPGAGV	LQ.....G		
adam12		M-----	-----AARP	LPVSPARALL	LALAGALLAP	CEARGVSLWN		
adam19		-----	-----	-----	-----	-----		
adam15		M-----	-----RLALLW	ALGLLGAGSP	LPSWPLPNIG	GTEEQQAESE		
adam8		M-----	-----RGLG	LWLLGAMMLP	AIAPSRPWAL			
		Pro-domain →						
		51				100		
adam28		VKKYEVVYPI	RLHPLHKREA	KEPEQQEQFE	TELKYKMTIN	GKIAVLYLKK		
adam7		-----	-----	-----	-----	-----		
gene216b		HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK		
gene216c		HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK		
gene216a		HIPGQPVTPH	WVLDGQPWRT	VSLEEPVSKP	DMGLVALEAE	GQELLLLELEK		
adam12		EGRADDEVSA	SVRSGLDWIP	VKSFD SKNHP	EVLNIRLQRE	SKELIINLER		
adam19		-----	-----	-----	-----	-----		
adam15		KAPREPLEPQ	VLQDDL.P.IS	LKKVLQTSLP	EPLRIKLELD	GDSHILELLQ		
adam8		MEQYEVVLP	RLPGPRVRR	LPSHLGL.HP	ERVS YVLGAT	GHNFTLHLRK		
		101				150		
adam28		NKNLLAPGYT	ETYYNSTGKE	ITTSP...QI	MDDCYQGH	LNEKVS DASI		
adam7		-----	-----	-----	-----	-----		
gene216b		NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL		
gene216c		NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL		
gene216a		NHRLAPGYI	ETHYGPDGQP	VVLAPNHT..	.DHCHYQGRV	RGFPDSWVVL		
adam12		NEGLIASSFT	ETHYLQDGT	VSLARNYTVI	LGH CYHGHV	RGYSDS VSL		
adam19		-----	-----S	GNPQTTRKL	EDHCFYHGT	RETELSSVTL		
adam15		NRELVPGRPT	LVWYQPDGTR	VV...SEGHT	LENCCYQGRV	RGYAGSWVSI		
adam8		NRDLLGSGYT	ETYTAANGSE	VTEQP...RG	QDHCLYQGHV	EGYPDS AASL		
		Cysteine switch						

	251				300
adam28	YNENQDEIRK	RVFEMANYVN	MLYKKLNTHV	ALVGMEIWD	KDKIKITPNA
adam7	NGHPHNKLRL	RIWGMVNFVN	MIYKTLNIHV	TLVGIEIWDH	EDKIELYSNI
gene216b	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
gene216c	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
gene216a	RHRNLNHTKQ	RLLEVANYVD	QLLRTLDIQV	ALTGLEVWTE	RDRSRVTQDA
adam12	QGKDLEKVKQ	RLIEIANHVD	KFYRPLNIRI	VLVGVEVWND	MDKCSVSQDP
adam19	NRRDQDATKH	KLIEIANYVD	KFYRSLNIRI	ALVGLEVWTH	GNMCEVSENP
adam15	KYRDFQHLLN	RTLEVALLLD	TFFRPLNVRV	ALVGLEAWTQ	RDLVEISPNP
adam8	LGSEA.AVRH	RVLEVNVHVD	KLYQKLNFRV	VLVGLEIWN	QDRFHVSPDP
	301				350
adam28	SFTLENFSKW	RGSVLSRRKR	HDIAQLITAT	ELAGTTVGLA	FMSTMCS.P.Y
adam7	ETTLRLFSFW	QEKILKTRKD	FDHVVLLSGK	WLYSHVQGIS	YPGGMCLPYY
gene216b	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
gene216c	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
gene216a	NATLWAFLOW	RRG.LWAQRP	HDSAQLLTGR	AFQGATVGLA	PVEGMCRAES
adam12	FTSLHEFLDW	RKMKLLPRKS	HDNAQLVSGV	YFQGTIGMA	PIMSMCTADQ
adam19	YSTLWSFLSW	RR.KLLAQKY	HDNAQLITGM	SFHGTITGLA	PLMAMCSVYQ
adam15	AVTLENFLHW	RRALLPLRLP	HDSAQLVTGT	SFSGPTVGMA	IQNSICSPDF
adam8	SVTLENLLTW	QARQRTTRHL	HDNVQLITGV	DFTGTTVGFA	RVSAMCS.HS
	351		Metalloprotease domain		400
adam28	SVGVVQDHS	NLLRVAGTMA	HEMGNHFGMF	HDDYSCKC..PSTICV
adam7	STSIKDLLP	DTNIIANRMA	HQLGHNLMGQ	HDEFPCCT..PSGKCV
gene216b	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
gene216c	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
gene216a	SGGVSTDHSE	LPIGAAATMA	HEIGHSLGLS	HD..PDGCCV	EAAAESGGCV
adam12	SGGIVMDHSD	NPLGAAVTLA	HELGNHFGMN	HDTLDRGCSC	QMAVEKGCCI
adam19	SGGVNMDHSE	NAIGVAATMA	HEMGNHFGMT	HDSAD...CC	SASAADGGCI
adam15	SGGVNMDHST	SILGVASSIA	HELGHSLGLD	HDLPGNSCPC	PGPAPAKTCI
adam8	SGAVNQDHSK	NPVGVACTMA	HEMGNHLMGD	HDENVQGCRC	QERFEAGRCI
	"Met-turn"				450
adam28	MDKALSFIYP	TDFSSCSRLS	YDKFFEDKLS	NCLFNAPLPT	DIISTPICGN
adam7	MDSDGSI.PA	LDLSKCRQNO	YHQYLKDYKP	TCMLNIPFPY	NFHDFQFCGN
gene216b	MAAATGHPFP	RVFSACSRRQ	LRAFFRKGGG	ACLNSAPDPG	LPVPPALCGN
gene216c	MAAATGHPFP	RVFSACSRRQ	LRAFFRKGGG	ACLNSAPDPG	LPVPPALCGN
gene216a	MAAATGHPFP	RVFSACSRRQ	LRAFFRKGGG	ACLNSAPDPG	LPVPPALCGN
adam12	MNASTGYFPF	MVFSSCSRKD	LETSLEKMG	VCLFNLPFVR	ESFGGQCKGN
adam19	MAAATGHPFP	KVFNGCNRR	LDRLYQSGGG	MCLSNMPDTR	MLYGGRRCCN
adam15	MEASTDFLPG	LNFSNCSRRA	LEKALLDGMG	SCLFERL.PS	LPMAAFCCGN
adam8	MAGSIGSSFP	RMFSDCSQAY	LESFLERPQS	VCLANAPDLS	HLVGGPVCCGN
	451		Disintegrin domain		500
adam28	QLVEMGEDCD	CGTSEECTNI	CCDAKTCKIK	ATFQCAL.GE	CCEKCQFKKA
adam7	KKLDEGEEDC	CGPAQECTNP	CCDAHTCVLK	PGFTCAE.GE	CCESCQIKKA
gene216b	GFVEAGEECD	CGPGQECDRL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
gene216c	GFVEAGEECD	CGPGQECDRL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
gene216a	GFVEAGEECD	CGPGQECDRL	CCFAHNCSLR	PGAQCA.HGD	CCVRCCLKPA
adam12	RFVEEGEEDC	CGEPEECMNR	CCNATTCTLK	PDAVCA.HGL	CCEDCQLKPA
adam19	GYLEDGEEDC	CGEEECNNP	CCNASNCTLR	PGAECA.HGS	CCHQCKLLAP
adam15	MFVEPGEQCD	CGFLDDCVDP	CCDSLTCQLR	PGAQCASDGP	CCQNCQLRPS
adam8	LFVERGEQCD	CGPPEDCRNR	CCNSTTCQLA	EGAQCA.HGT	CCQECKVKPA

	501		550
adam28	GMVCRPAKDE	CDLPEMCNGK	SGNCPDDRFO VNGFPCHHGK GHCLMGTCPT
adam7	GSICRPAKDE	CDFPEMCTGH	SPACPKDQFR VNGFPCKNSE GYCFMGKCPT
gene216b	GALCRQAMGD	CDLPEFCTGT	SSHCPD V YVL LDGSPCARGS GYCWDGACPT
gene216c	GALCRQAMGD	CDLPEFCTGT	SSHCPD V YVL LDGSPCARGS GYCWDGACPT
gene216a	GALCRQAMGD	CDLPEFCTGT	SSHCPD V YVL LDGSPCARGS GYCWDGACPT
adam12	GTACRDSSNS	CDLPEFCTGA	SPHCPANVYL HDGHSCQDVD GYCYNGICQT
adam19	GTLCREQARQ	CDLPEFCTGK	SPHCPTNFYQ MDGTPCEGGQ AYCYNMCLT
adam15	GWQCRPTRGD	CDLPEFCPGD	SSQCPPDVSL GDGEPCAGGQ AVCMHGRCAS
adam8	GELCRPKKDM	CDLEEFCDGR	HPECPEDAFQ ENGTPCSGG. .YCYNGACPT
Cysteine rich domain			
			600
adam28	LQEQCTELWG	PGTEVADKSC	YNR.NEGGSK YGYC.RRVDD TLIPCKANDT
adam7	REDQCSELF	DEAIESHDIC	YKM.NTKGNK FGYC.KNKEN RFLPCEEKDV
gene216b	LEQQCQQLWG	PGSHPAPEAC	FQVVNSAGDA HGNCGQDSEG HFLPCAGRDA
gene216c	LEQQCQQLWG	PGSHPAPEAC	FQVVNSAGDA HGNCGQDSEG HFLPCAGRDA
gene216a	LEQQCQQLWG	P.....
adam12	HEQQCVTLWG	PGAKPAPGIC	FERVNSAGDP YGNCGKVS KS SFAKCEMRDA
adam19	YQEQCQQLWG	PGARPAPDLC	FEKVNVA GDT FGNCGKVMNG EHRKCNMRDA
adam15	YAQQCQSLWG	PGAQPAAPLC	LQTANTRGNA FGSCGRNPSG SYVSCTPRDA
adam8	LAQQCQAFWG	PGGQAAEESC	FSYDILPG.. .CKASRYRAD
	601		650
adam28	MCGKLFCQGG	S.DNL P WKGR	..IV..... .TFLTCKTFDPED
adam7	RCGKIYCTGG	ELSSLLGEDK	..TYHLKDPQ KNATVKCKTIFLYH
gene216b	LCGKLQCQGG	KP.SLLAPHM	VPVDSTVHL. DGQEVTCRGA LAL..PSAQL
gene216c	LCGKLQCQGG	KP.SLLAPHM	VPVDSTVHL. DGQEVTCRGA LAL..PSAQL
gene216a	DGQEVTCRGA LAL..PSAQL
adam12	KCGKIQCQGG	ASRPVIGTNA	VSIETNIPLQ QGGRILCRGT HVYLG....D
adam19	KCGKIQCQSS	EARP.LESNA	VPIDTTI.IM NGRQIQCRGT HVYRGPEEEG
adam15	ICGQLQCQTG	RTQPLLGSIR	DLLWETIDV. NGTELNC S WV HLDLGS....
adam8	MCGVLQCKGG	QQPLGRAICI	VDVCHALTTE DGTAYE.....
EGF-like domain			
	651		700
adam28	TSQEIGMVAN	GTKCGDNKVC	INAECVDIEK AYKSTNCSSK CKGHAVCDHE
adam7	DSTDIGLVAS	GTKCGEGMVC	NNGECLNMEK VYISTNCPSQ CNENPVDGHG
gene216b	DLLGLGLVEP	GTQCGPRM..VCNSN.
gene216c	DLLGLGLVEP	GTQCGPRMVC	QSRRRCR K NA. FQELQRCLTA CHSHGVCNSN
gene216a	DLLGLGLVEP	GTQCGPRMVC	QSRRRCR K NA. FQELQRCLTA CHSHGVCNSN
adam12	DMPDPGLVLA	GTKCADGKIC	LNRQCQNIS. VFGVHECAMQ CHGRGVCNNR
adam19	DMLNPGLVMT	GTKCGYNHIC	FEGQCRNTS. FFETEGCGKK CNHGVCNNN
adam15	DVAQPLLTL	GTACGPGLVC	IDHRCQRVD. LLGAQE C RSK CHGHGVCDSN
adam8PVPE	GTRCGPEKVC	WKGRCDLH. VYRSSNCSAQ CHNHGVCN H K
Transmembrane			
	701		
adam28	LQCQCEEGWI	PPDCDDSSVV	FHFSIVVGVL FPM A VIFVVV AMVIRHQSSR
adam7	LQCHCEEGQA	PVACEETLHV	TNITILVVVL VLVIVGIGVL ILLVRYRKCI
gene216b	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ AENHDTFLLA MLLSVLLPLL
gene216c	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ AENHDTFLLA MLLSVLLPLL
gene216a	HNCHCAPGWA	PPFCDKPGFG	GSMD.SGPVQ AENHDTFLLA MLLSVLLPLL
adam12	KNCHCEAHWA	PPFCDKPGFG	GSTD.SGPIR QA E ARQEAAE SNRERGQ Q E
adam19	QNCHCLPGWA	PPFCNTPGHG	GSID.SGPM. PPESVGPVVA GVLVAILVLA
adam15	RHCYCEEGWA	PPDCTTQLKA	TSSL.TTGLL L.SLLVLLVL VMLGAGYWYR
adam8	QECHCHAGWA	PPHCAKLLTE	VHAA.SGSLP VLVVVVLVLL AVVLVTLAGI

FIG. 11C

	Domain →	Cytoplasmic domain → 800			
adam28	EKQKKDQRPL STTGTRPHKQ	KRKPQMVKAV	QPQEMSQMKP	HVYDLPVEGN	
adam7	KLKQVQSPPT ETLGVENKGY	FGDEQQIRTE	PILPEIHFLN	KPASKDSRGI	
gene216b	PGAGLAWCCY RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
gene216c	PGAGLAWCCY RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
gene216a	PGAGLAWCCY RLPGAHLQRC	SWGCRDPAC	SGPKDGPHRD	HPLGGVHPME	
adam12	PVGSQEHAASLTLI----	-----	-----	-----	
adam19	VLMLMYCCCR QNNKLGQLKP	SALPSKLRQQ	FSCPFRVSQN	SGTGHANPTF	
adam15	ARLHQRLCQL KGPTCQYRAA	QSGPSERPGP	PQRALLARGT	KSQGPAPKPPP	
adam8	IVYRKARSRI LSRNVAPKTT	MGRSNPLFHQ	AASRVPAKGG	APAPSRGPQE	
	801				Putative SH ₂
adam28	EPPASFHKDT NALPPTVFKD	NPMSTPKDSN	PKA-----	-----	
adam7	ADPNQSAK--	-----	-----	-----	
gene216b	LGPTATGQPW PL.....DPENSHEPS	SHPEKPLPAV	
gene216c	LGPTATGQPW PLAPGSPADH	IHNIYPPPFLL	PDPENSHEPS	SHPEKPLPAV	
gene216a	LGPTATGQPW PL.....DPENSHEPS	SHPEKPLPAV	
adam12	-----	-----	-----	-----	
adam19	KLQTPQGKRK VINTPEILRK	PSQPPPRPPP	DYLRGGSPPA	PLPAHLSRAA	
adam15	PRKPLPADPQ GRCPSGDLPG	PGAGIPPLVV	PSRPAPPPPT	VSSLYL----	
adam8	LVPTTHPGQP ARHPASSVAL	KRPPPAPPVT	VSSPPFPVPV	YTRQAPKQVI	
	851				900
	binding domain				
adam28	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	
gene216b	SPDPQADQVQ MPRSCLW----	-----	-----	-----	
gene216c	SPDPQADQVQ MPRSCLW----	-----	-----	-----	
gene216a	SPDPQADQVQ MPRSCLW----	-----	-----	-----	
adam12	-----	-----	-----	-----	
adam19	RNSPGPGSQI ERTESSRRPP	PSRPIPPAPN	CIVSQDFSRL	RPPQKALPAN	
adam15	-----	-----	-----	-----	
adam8	KPTFAPPVPP VKPGAGAANP	GPAEGAVGPK	VALKPPIQRK	QGAGAPTAP--	
	901				950
adam28	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	
gene216b	-----	-----	-----	-----	
gene216c	-----	-----	-----	-----	
gene216a	-----	-----	-----	-----	
adam12	-----	-----	-----	-----	
adam19	PVPGRRSLPR PGGASPLRPP	GAGPQOSRPL	AALAPKVSPR	EALKVKAGTR	
adam15	-----	-----	-----	-----	
adam8	-----	-----	-----	-----	
	951				990
adam28	-----	-----	-----	-----	
adam7	-----	-----	-----	-----	
gene216b	-----	-----	-----	-----	
gene216c	-----	-----	-----	-----	
gene216a	-----	-----	-----	-----	
adam12	-----	-----	-----	-----	
adam19	GLQGGRCRVE KTKQFMLLVV	WTELPEQKPR	AKHSCFLVPA	-----	
adam15	-----	-----	-----	-----	
adam8	-----	-----	-----	-----	

FIG. 11D

mGene216	MGSRCGRPGG	SPVLLLLLPLL	LPSCLPLRSAR	MFPASIPKPH	LHIPTCTWLT	50
Gene 216c	MGWR	-----	-----F-RRAR	-----GTP	-----	12
Gene 216b	MGWR	-----	-----F-RRAR	-----GTP	-----	12
Gene 216a	MGWR	-----	-----F-RRAR	-----GTP	-----	12
mGene216	NYEAHVTLRT	RFLPLLLFQI	LKMYMSVLPA	HASVYRGNA	HG-----	92
Gene 216c	-----	---T-LLLLLL	LLIW--FVPG	-AGVLQ-GED	AGGVPLTLC	45
Gene 216b	-----	---T-LLLLLL	LLIW--FVPG	-AGVLQ-GHI	PG-----	37
Gene 216a	-----	---T-LLLLLL	LLIW--FVPG	-AGVLQ-GHI	PG-----	37
mGene216	-----E	LVTPHWILEG	RLWLKVTLEE	PILKPDVSLV	ALEAEGDILL	133
Gene 216c	VFTPGHIPGQ	FVTPHWVLDG	QFWRTVSLEE	PVSKPDMGLV	ALEAEGQELL	95
Gene 216b	-----Q	FVTPHWVLDG	QFWRTVSLEE	PVSKPDMGLV	ALEAEGQELL	78
Gene 216a	-----Q	FVTPHWVLDG	QFWRTVSLEE	PVSKPDMGLV	ALEAEGQELL	78
mGene216	LELEKKHKLL	APGYIETHYR	PDGHPVVLSP	NHTDHCQYHG	RVRGFRESWV	183
Gene 216c	LELEKNHRL	APGYIETHYG	PDGQPVVLAP	NHTDHCHYQG	RVRGFEDSWV	145
Gene 216b	LELEKNHRL	APGYIETHYG	PDGQPVVLAP	NHTDHCHYQG	RVRGFEDSWV	128
Gene 216a	LELEKNHRL	APGYIETHYG	PDGQPVVLAP	NHTDHCHYQG	RVRGFEDSWV	128
mGene216	VLTCSGMSG	LITLSRNASY	YLREWPPRGS	KDFSTHEIFR	MEQLITWKGT	233
Gene 216c	VLTCSGMSG	LITLSRNASY	YLREWPPRGS	KDFSTHEIFR	MEQLITWKGT	195
Gene 216b	VLTCSGMSG	LITLSRNASY	YLREWPPRGS	KDFSTHEIFR	MEQLITWKGT	178
Gene 216a	VLTCSGMSG	LITLSRNASY	YLREWPPRGS	KDFSTHEIFR	MEQLITWKGT	178
mGene216	QRDKNSQYKA	GMASLEHVPQ	SRGRREARRS	RYLELYIVA	DHTLV----	278
Gene 216c	CGHRDEGNKA	GMTSLFGGPQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	245
Gene 216b	CGHRDEGNKA	GMTSLFGGPQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	228
Gene 216a	CGHRDEGNKA	GMTSLFGGPQ	SRGRREARRT	RKYLELYIVA	DHTLFLTRHR	228
mGene216	SPSDSD	---SGY----	TVVDRA-G	SVD-RAGGS	HHSGRKRNA	314
Gene 216c	NLAHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	295
Gene 216b	NLAHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	278
Gene 216a	NLAHTIKORLL	EVANYVDQLL	RTLDIQVALT	GLEVWTERDR	SRVTQDANAT	278
mGene216	L-GF-----	-----PT---	-----VAFR--	G-----VG---	QE TTRLHTT---	335
Gene 216c	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	345
Gene 216b	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	328
Gene 216a	LWAFLOWRRG	LWAQRPHDSA	QLLTGRAFCG	ATVGLAPVEG	MCRABSSGGV	328
mGene216	AHDHSELPIG	TAATMAHEIG	HSLGLSHDPD	GCCVQADAEQ	GGCVMEAAATG	385
Gene 216c	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	395
Gene 216b	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	378
Gene 216a	STDHSELPIG	AAATMAHEIG	HSLGLSHDPD	GCCVEAAAES	GGCVMAAATG	378
mGene216	HPFPRVFSAC	SRQLRTFFR	KGGGPCLSNT	SAPGLLVLP	RCNGFLEAG	435
Gene 216c	HPFPRVFSAC	SRQLRAFFR	KGGGACLSNA	PDPGLPVPPA	LCNGFVEAG	445
Gene 216b	HPFPRVFSAC	SRQLRAFFR	KGGGACLSNA	PDPGLPVPPA	LCNGFVEAG	428
Gene 216a	HPFPRVFSAC	SRQLRAFFR	KGGGACLSNA	PDPGLPVPPA	LCNGFVEAG	428
mGene216	EECDCGSGQ	-----	-----	-----L	KSAGTPCRFA	455
Gene 216c	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCRCA	495
Gene 216b	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCRCA	478
Gene 216a	EECDCGPGQE	CRDLCCFAHN	CSLRPGAQCA	HGDCCVRCIL	KPAGALCRCA	478

FIG. 12A

mGene216	ATDCDLPEFC	TGTSPYCPAD	VYLLDGSPCA	EGRGYCLDGW	CPTLEQQCQQ	505
Gene 216c	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	545
Gene 216b	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	528
Gene 216a	MGDCDLPEFC	TGTSSHCPPD	VYLLDGSPCA	RGSGYCWDCG	CPTLEQQCQQ	528
mGene216	LWGPFGSKPAP	EPCFQOMNSM	GNSQGNCGQD	HKGSFLPCAQ	RDALCGKLLC	555
Gene 216c	LWGPFGSHPAP	EACFQVVNSA	GDAHGNCGQD	SEGHFLPCAG	RDALCGKLQC	595
Gene 216b	LWGPFGSHPAP	EACFQVVNSA	GDAHGNCGQD	SEGHFLPCAG	RDALCGKLQC	578
Gene 216a	LWGPFGQ---	-----	-----	-----	-----	535
mGene216	QGGEPNPLVP	HIVTMDSTIL	LEGREVCRCG	AFVLPDSHLD	QLDLGLVEPG	605
Gene 216c	QGGKPSLLAP	HMVPVDSTVH	LDGQEVTCRG	ALALPSAQLD	LLGLGLVEPG	645
Gene 216b	QGGKPSLLAP	HMVPVDSTVH	LDGQEVTCRG	ALALPSAQLD	LLGLGLVEPG	628
Gene 216a	-----	-----	---EVT---	ALALPSAQLD	LLGLGLVEPG	561
mGene216	TQCGPRM---	-----	-----	-----	-----P	613
Gene 216c	TQCGPRMVCQ	SRRCRKNAFQ	ELQRCLTACH	SHGVCNSNHN	CHCAPGWAPP	695
Gene 216b	TQCGPRMVCN	SNHNCHCA--	-----	-----	----PGWAPP	652
Gene 216a	TQCGPRMVCQ	SRRCRKNAFQ	ELQRCLTACH	SHGVCNSNHN	CHCAPGWAPP	611
mGene216	--HGP-LANS	VRTLHLLTCS	QT--LRTLSL	PKNYPL---	-----KCP	647
Gene 216c	FCDKPGFGGS	MDSGFVQAEH	HDTEILLAMLL	SVLLPL---	-----LP	733
Gene 216b	FCDKPGFGGS	MDSGFVQAEH	HDTEILLAMLL	SVLLPLLPGA	GLAWCCYRIP	702
Gene 216a	FCDKPGFGGS	MDSGFVQAEH	HDTEILLAMLL	SVLLPLLPGA	GLAWCCYRIP	661
mGene216	GLQIEF----	-----	-----QTC-	-PI--PMRED	K-CAL-PCDL	671
Gene 216c	GAGLAWCCYR	LPGAHLQRC	WGCRDRFACS	GPKDGEHRDH	PLGGVHPEMEL	783
Gene 216b	GAHLQRC----	-----S	WGCRDRFACS	GPKDGEHRDH	PLGGVHPEMEL	740
Gene 216a	GAHLQRC----	-----S	WGCRDRFACS	GPKDGEHRDH	PLGGVHPEMEL	699
mGene216	--QSSVSQT--	-----	-----	HSYNSY--GL	YAEILLSIGT	696
Gene 216c	GPTATGQPWP	LAPGSPADHI	HNIYPPPFLP	DPENSHEPSS	HPEKFLPAVS	833
Gene 216b	GPTATGQPWP	L-----	-----	DPENSHEPSS	HPEKFLPAVS	771
Gene 216a	GPTATGQPWP	L-----	-----	DPENSHEPSS	HPEKFLPAVS	730
mGene216	PEP--DHV--V--SR--LP					707
Gene 216c	PDPQADQVQM	PRSCILW				849
Gene 216b	PDPQADQVQM	PRSCILW				787
Gene 216a	PDPQADQVQM	PRSCILW				746

FIG. 12B

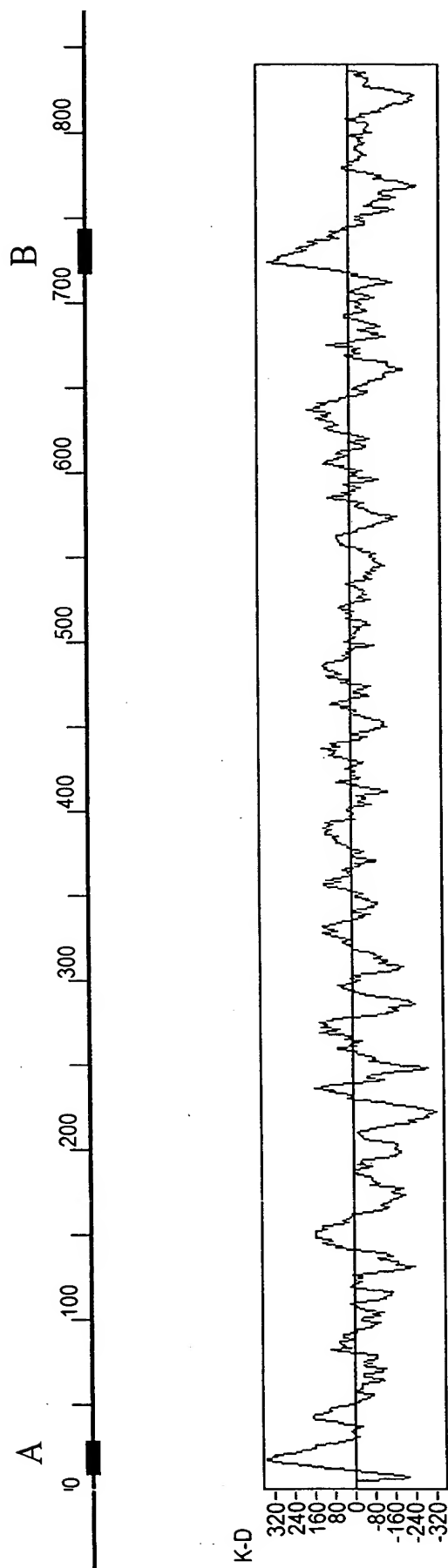


FIG. 13

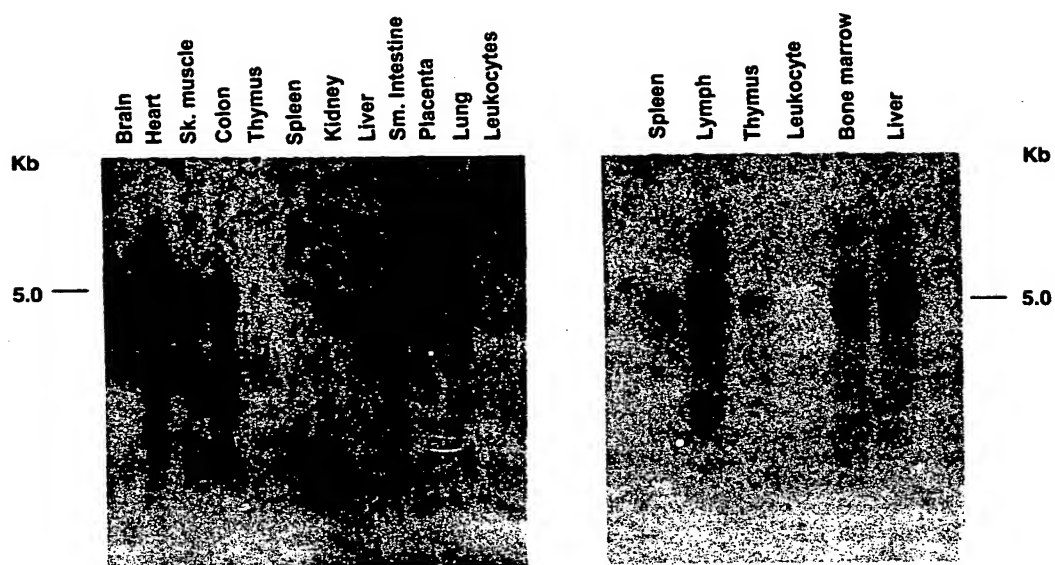


FIG. 14

Gene_216: Transcript A

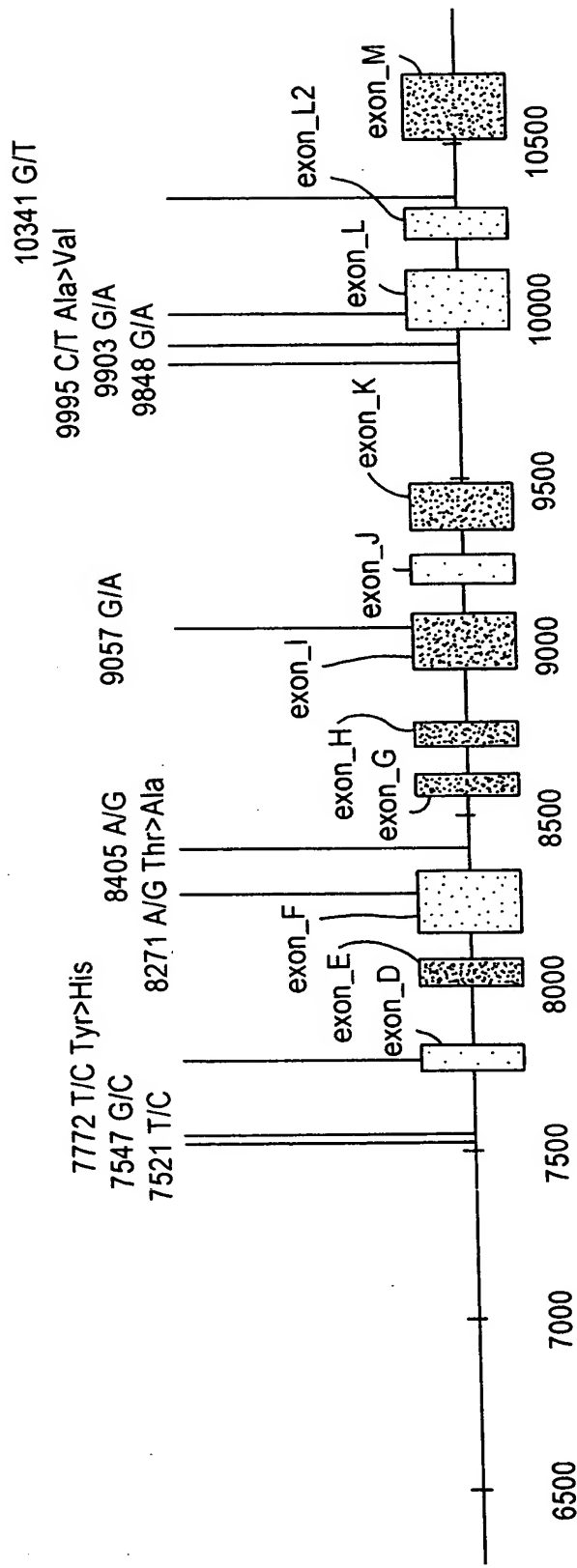
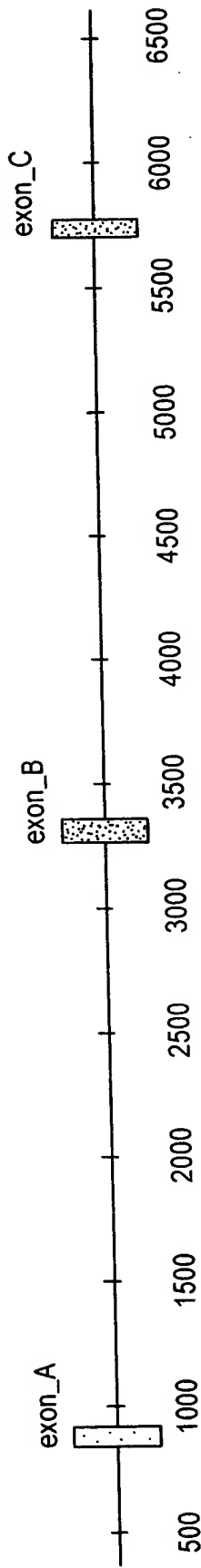


FIG. 15A

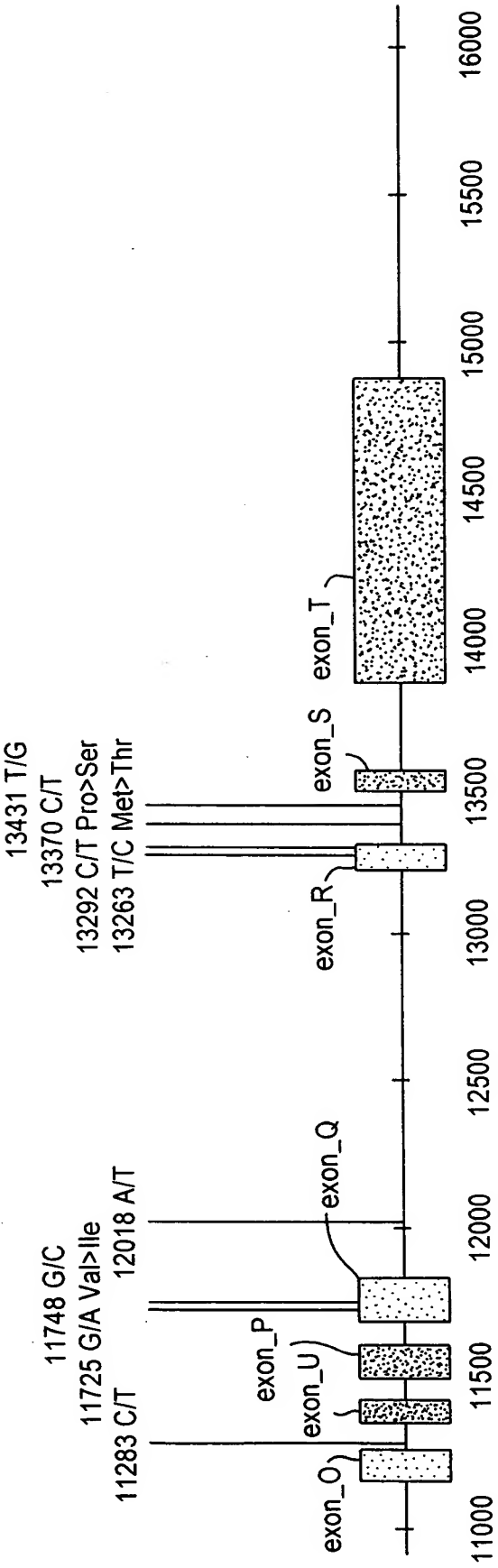


FIG. 15B

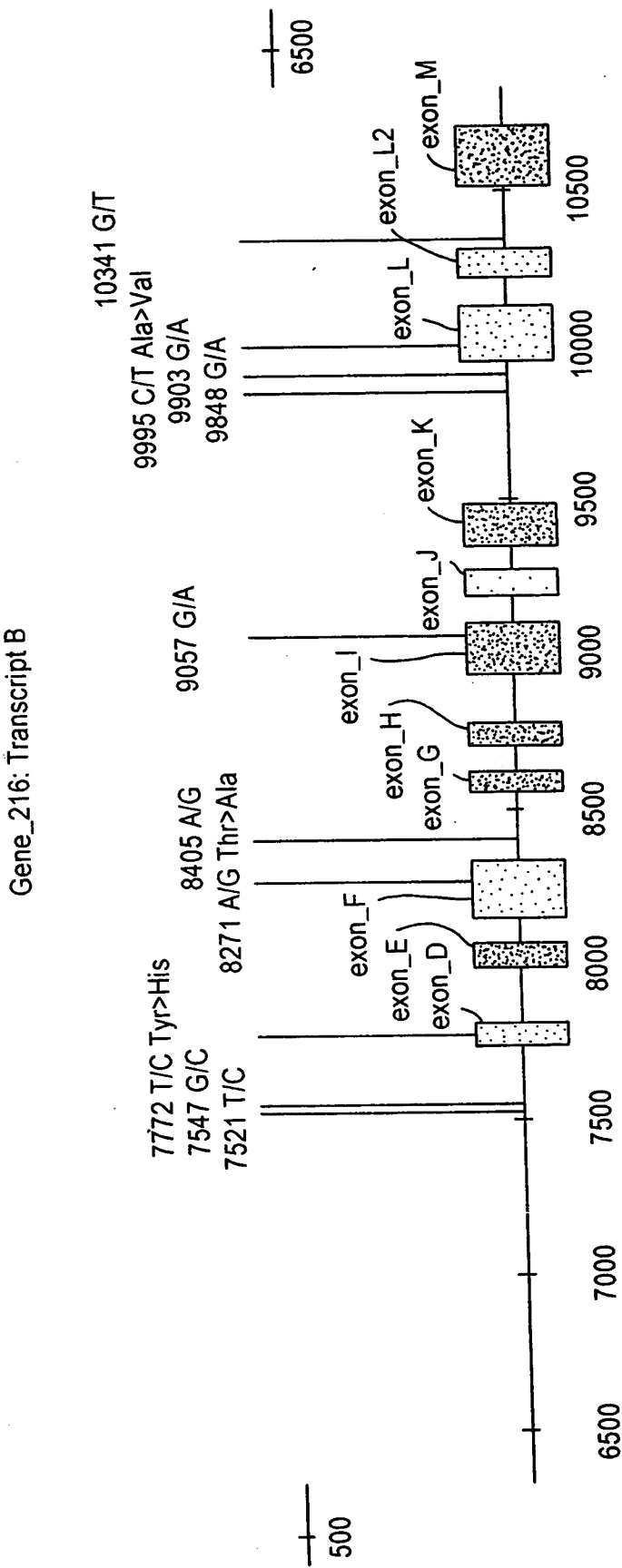


FIG. 16A

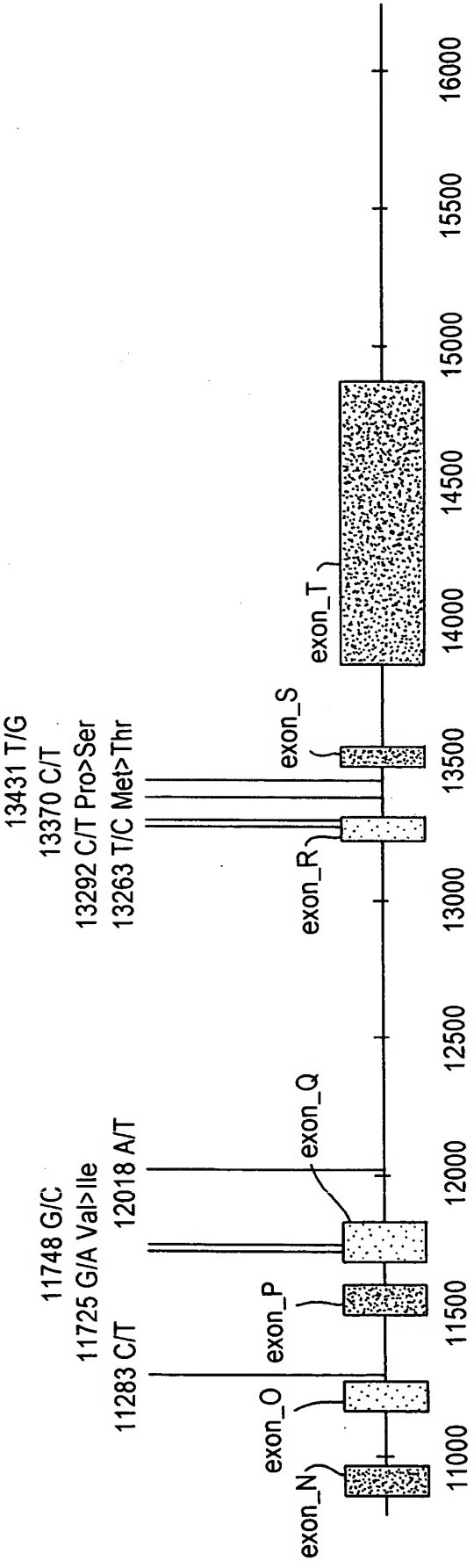


FIG. 16B

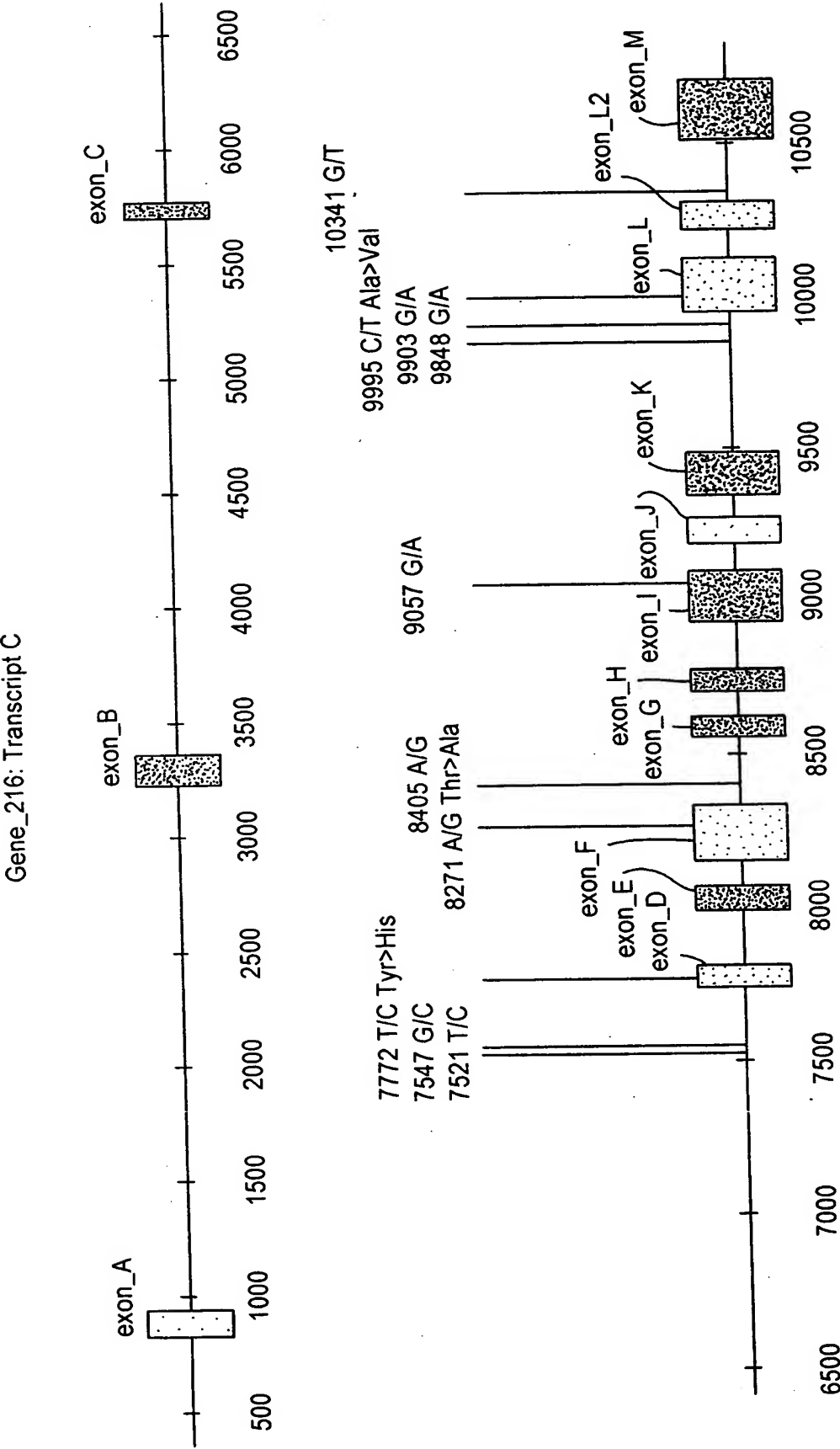


FIG. 17A

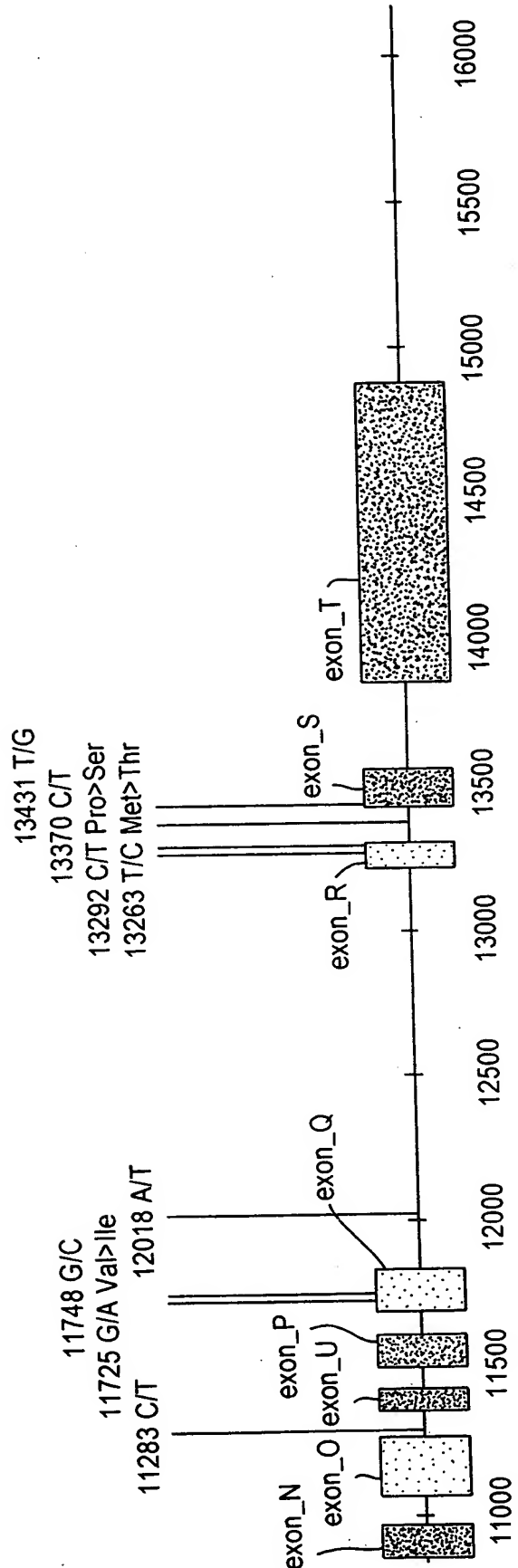


FIG. 17B

>Mouse 216 homologue genomic DNA sequence
CACAAATATATACACATGGTAAGTGTATTAGCAAAATGGCTTTCTATGTAATATAAAATAAG
ATAAAAAAACAAACAAACAAAAACAAAACCAGAAATACCAGCACTTCAGAGTACCCAC
TCCCAACCCCTGCCAGTGTAGCTGCTAACTTCACCTAATCAAGTTAATTTAAAAATCAAA
TATAATACCACAGATTTTATTTTCTGTGTTTCTGCTTTATACAAATGGTATCATATTT
TAAACATGAGAACATTGTGAGATGACTAGCCAGTGTCTGTCTGTCTGTCTCTCAGATA
TTTATTTATTTATTTTATGTATGTAGGTACACTGTCACGTCTTTCAGACACACCAGAAGA
GGACATTGGATCCCATTACAGATGGTTGTGAGCCACCATGTGGTTGCTGAGAATTGAACT
CAGGACCTCTGGAAGAGTAGTCAGTGCTCTTAACCACTGGGCCATCTTTCCAGTCTGAC
CAGTGTCTCTTAATGGTGAAATATTCTTCCCTTGGCCCTAGCATTATCCTTGGGCATT
TTCTCAGGAAAAATGAAGGCGCGTGTACCCCTGAGATTTGTTACTAGGATGTTTCATAACA
GTGCTACCCATCAGCCAGGAAGTGAACAAATAAATGCTCGGCAGCAGGGGAATGACCGA
GTAGACAGAGCTACGCCCACACAGCTATGAGAGCTGTGCCTACAGCTGAGTGTGGTTCTC
AGACGGTCAGTGGGAGGGGCTGGCAGCGATGGCTGCCTGTGGCAGTTACATGTCTACCG
CTCTATTAAAGGAGCTAACAAAGGCAACCTTAAGGAAGGAAACATTTATTTGGGTACAG
GTTAGTAGGCACAGTCTCAGAGTGGTTGGAAAGATGGCAGCAAGTGTCTCTAGCTGAGGG
GGCAGGAGTGGGAGGCCCTGGTCACTTTGTGTGCGCGAGGAAGCAGACAGAGAGGTGGGG
GTGCCGTTTGCTTCTTACTTTCCTCTTCTACCCAGTCCAGGATGACAGAACATCAGGTA
TTGCCACCCACATTTGGAGTGGGTCTTCTGGTCTCTGTAAACTCTCTGGAAACACCCCT
CACTGACCTGATGTGCCCCGGAACAAGGTGATTCTCAGCCCCAAGCAAGTCACAGCGAAGAC
CAAGGACAGGTATAGTTAAGGAATGGGATAGAAGTCAATACACAGCCACTGGTGGGCAAA
AGGGATGGGCGGGAGCACAAATGGAGATTGAGAGCCAGGGAAGTGAGCAGGTTCACTTTG
TGAAATCTCACATTTCTGAATCTATATTTTGGAAAGAAAACTTAATTTAAAAAAATCTG
CCACTTTTCTACGCCTTGTGCTGTGTATCGACATGGGAGGATACCTTGAGGCCAGGAGA
CTGAGATCAGCCTGAGCAACACAATAAAACCTCATTCTTACAAAACAGAACAAATTTGGG
TGTGGAGGTGCACGCCTTTAATCCCAGCACCCAGGGAGCAGAGCCAATCACCCCTTGTAAC
CATCTCAAATTCAGACCCAGGGGCTGTCTAGCGGCAGAAGAGTCCATGGAACACTGTGAC
CATAGTCATACAATTGGAACACTACTTATCGACAAGAATAAATGGCCATAGGTAATAGGCA
ATAGGTTGGGTAAACTCACAAATTGGGAAATACAACCCATACTCCAGACAAGGGCCAA
TCGCCTTTTAAACATAGAGGTCTTTAAACTGTTAAAGAAGGACCAACCACTCACTAGAA
AAATGAGCTACACATGAATATGTTACTATATTTAAAAAATAAATCCTGTGTCTAAAA
CAGCAGCTTATGTAAGAAATTTGGTAGTAGTGGCTTTCTGTGGGGAAGGAGTACCCAAAGG
ATGGAGACTAAAGGAAGACTCTCCTAAGCATTATTTATACCTTCTCCCTTGTTTGTCTTGT
GTAGTGGTGGTGGTTGTTTTTGATTCTTTTTTGTTTGGTTGGTTTTGGTTTTTTCAAGA
CAGTGTCTCTTGTGGAGCCCTGGTTGTCTGGAACCTCACTCAGGCTGCCCTTGAACCTCA
GAGATTCTCCTGCCTCTGGGCTTAAAGGTGTACCTCACCAGTGTGAGGCTTGGGTTTGT
TTTGAGACGGGGTCTTGCTGTGTAGCTCCAGCTGCCTCTGAAGTGCTAGAATTACAGACA
TGAACCTACAGATATCTCCAGTCTCCTCTCATTCTCCCTCCCTGCCCCCTTTGTATACAC
ATTACCTGTGTGTGCATGTGTGACTCACTCTGAGTTCTTCCAGTGTACTCTCCATCAG
ATTTTTTGAGATAGGGTCTCTTACTGAACCTGGACCTCAAACATTTGCCTGTCTCTGTCC
AGTCCAACTTGGCTTACAAGTTTGTGCAATGGTTCTGGCTTTCTCTGATTGTCTGGAGA
CTTGAACCTCAAGAACCAACGCAGGTCTTACTACTAAGCCTTCTCCTTGATGACACCC
CTCACCCCACTGCCACACACCAGGTCTCCAGGCTGATCTCACACTTTTTCCATATAGGAC
TTTGAACCTTGTCTTTTGCCTCTCTGCTGGGATACAGGTGTGTGCTGCTACACCCAATTTA
TGGGATGCTGGGGATGGAACCTCAGGGCCCCAATCTTGATCAACTGAGGTGCGCTCGCTC
TCTCGCTCTCATTCC
CCCTCCTTCCCTTCCCTCTCTCTTCCATGAGACTTCTTTCTATATTGCACAGGCTAGCTA
TCTTGAGTGTCTCTCTCGATCCAATTGCCTGACCTATCATACTGGTTTTCTGTTTTTGG
TTTTGGTTTTTTTCGAGACTGGGTTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCACTTT
GTAGACCAAGGCTGGCCTCGAACTCAGAAATCCGCCTGCCTCTGCCTCCCGAGTGTCTGGGA
TTAAAGGCGTGCACCAACACGCCTTTAATCCCAGCATTGTATGTTTCAATCGTATAAATG
TTTTTTCTTCTGCCGTTGGAACCTTTTACATTCCATATTCTCAGAACGAAATTTAATCA
TCTTATTTCAAAGTTAAATCTCTTGCTATCCGAAATCATACCAAGTGTACGAAGTGATCT
TTTCAACACGAAAGCAATGTCTTAAATTTGGGAAAGGGTCCCTCATGCCTGGGGGTCT
GTGGTATAGAACAATTCTGTCTGGCCATCGCTGTTCTCTGCCCTGTGCCACCACTGC
ATTGCCCTTACCAGGAACCAAGACTTCAGCAACGCGGCCACCACAAGACCCCTAGGTAC

FIG. 18A

FIG. 18B

TCCTCCTGTCCCCAGATGTATTCTCACTCTGGTTTGCTTCTCCAGAGCCCTGCTCAGCCT
 CCTCCTAACTTCTGCTCATTGTGTTCCCCCAGAAGAGCCATGTGTGCCCTTCACTGCTTCG
 CTGCCCATGGGGAGGCCCGGCACTGATCCGCTGGCTTACAGAGAGGCAAGCGAGCCCCAC
 AGAGCTTGTAAGTTGCTCATGCTTGAATAGTTTATTGGGCCCTAGAAACCTGAGGCTCCG
 TGGGACCTAAGGGCTTCAGATGATTGGCTGCCCTCCCCTTCTTTCTATACTACTCAGGC
 TGGAGAGAGTTCAATTCTGTACCTCCTGACAGAGGGCAGCCCCACTGTCCAAACCTAGAG
 TGTGCAACAGTGAGGATGCATTCCCAGAAACCTAAACCTTCCAAGTCAGGGCCTTCACT
 GGGGTCCCCCAGACTTCTAGGACTTCTCTCAACCAAGCAAAGATGGCTTGTGGACATGCA
 CGGGTTCCTTGATGGTGGCCTCTCTCCTTGCCCTGGCTCGGTCTGTGAGAGAATCCCAGG
 GGGACTCTGCTCTGCGTTAGGAAGCCTGTGAGGCCAGGCCAGGAAGAGCTTTGGCAGGGT
 GTGTGTATTTACAAACAGGGTTGTACTGCAGGATGGGGATGGTGCACAAAGGGGGAGGG
 AGACCTTGGAGCAGAAGTAAAGGCAGCAAGGGCCGAGAGGGAAGGGACCTTCCACTGGG
 GCTACTGCCTTTCTCCAGAGCAGACATTTTCCATAAAGCAAGAGGCACCTCCAACCTATA
 TAAGCTCATGTTTGGGCCCTTGTGGAGCCTGTGGCTGGGGAAAGTGAGGGCCATCTTCTCT
 ACACCTGCTGCAGAAGGGCCCTGAAAGATTCTTGGCCAGGGTCCCAGCCCAGTGCATTTT
 GGGATAAAAAGGGAAAGCCATCGTGGGTGGGGAAAACATTTAAAAAAAATAACAGCAGC
 CTCCCCTGGAATCTCTTGGGCTAGTTCCAGTTCTGGCTTCTAGCCAGGCTAAGTGGACTA
 GCCTGAGAGAGACCAAGTCAGTGAGAGAGGAGAGGTGGCTAGAGGGCCAAGGCCAGCCCT
 TCTGACATCTAGCTAAGAGAGTCAACACTTTTTAGGGAGCCAAAGTTGGGTTTCACTGTTT
 ACTTCATGAGTTTCAAGTTATGAGGCCAGCTCAGAGGAATTTTCAAGAGGATCGGGCAGTTTGT
 CAGAACTGAAGGTGGAGGAAAAGTTTGGGTTCTCTCAGGAATGAGGGAAAGGCAGCAAG
 ATGGAGAGATGTGCAACCAGGAGCTGTGGATGCAGCTGGGTGATTTGGTGTCTGCTTGGC
 ATGTGCAAGGCCCTGGGTTTGATCTATAGCACCCACAGCAAACTAGCAAGCAAGCAAAACA
 AGCATACAAACAAAACAGAAGCAAGGTTGCAGGTAGTACAAGAGATGGCCAAAGCTGTAG
 CCCACCCAATGACCCACATCACCTCAGTGCCCACTGCCTCCTGCTTTTCTGCTTTTCTC
 ATGGGGCTCCTGACTATGGCCATAGCATATGTCCATAGCAGACATAACAACATATGCCAG
 GCAACGTAGCAACTGCTATGTCCGTATATGGTGGTTATGCATCTTTAAGGGTCCGTTGTC
 ACAAACACAAGCACTGAGAACATCTCTAAGTTACAACCTCCACACATATCCACTCCCTGC
 AATGCGAGAGCCAGCTGTTTCTATGAGCTTTCTCACTAGGCAGCTCTACATCCTACCGGT
 TCCTGGGCAGCCAGGTGGCCTTGGGGCCTAGTGTGTCACTGCGTTTCTTCTCGGTGAGAT
 CTTGAAGCCTGACTCGGTGCTGGTGGCTTTAGAGGCTGAAGGCCAGGATCTCCTGCTTGA
 ACTGGAGAAGAAGCAGTGAGTACCAGCGGGGGGGTTGCTGAAGTCCAGACAAAGACCCTC
 TCTGGAGAGGATCAGTGCTTTCTGGGAGGGGGTTGGGGGCTGGGTGGGAAGCAGCAGTGG
 GAGTGACAGGGAGAGTGGCGGATGTACTTGGGGCTACAGTGGACTGAACCCAACTGTAGG
 AAGTACATACCTGGTCATCTCATACCCTGGAGCAGCTGGATGGGCGGCTCCCCGCTGGAG
 AAGAGTGAGCACCAGAACAGACATTGACTGATACCTTAATTCAAAGGGAATTCTTAGGCA
 AAGGGAACCTCCACAGATGGCAGAAGAAAAGCTGCGAAGGTCAAATCCAATGGTGACAG
 TTCATCTGGTCTACCTGGAATGCCTCCATCTGCGTGGAAGAGAACAGAGACATCTGGTCT
 ACCTGGAATGCCTCCATCTGCGTGGAAGGGAACAGAGAGGAGAGGGCTGGGGTGGGGGGC
 TCCCCAGTGGGGCCGATCGAAGAGGGCATCTTAGTGCTAAAGATCTTGGATGGACCTAAA
 GAGTCAAAGAACGGGAGGTGGTAAAGGAGAAACACAGTGTGGAAGGAGTGAGAGGGTAA
 GCAAGATGGAGGCGTGAAGTGCAGACTCCACCACCAACCACCACTCGCTCATGTCTG
 CTTTCTTACGGACATTGCAAGGCACTCATTCAATTTATTCTCTCCATGGAATCAGACA
 GACTGGGAACAACTGCAACACCACGCCAAACCACAGTTCTGACAGTGCCACATCCCT
 TCCTACTAAACGGTCTTGTACATGTGTGCACACATTGAACGTTAGCATGTATGAGTGCAG
 CCAGCAAAGCAGCAGAGTTGTAATGTGTGTAAGGATGGCTGGCCGTACAACAGCCTGGGT
 TTTTGATGGAGGACAATGTGAATTTGGAGTCAGGATTTTCTGTAAGGAAGAGCAATTGAA
 GTCAGGCATGGAGGTAGAGGCCTGTAAGTCCGGCTCCTCTGGGCAGGAGAACACAGAGTC
 AAGTCAGGGACTGCCTGAGTTATAAAGAATGAGTTCAAGACCAGCCTAGGCAACTTAGCA
 AAATCCAGTCTCAAAATATAAAGGAGTGAGGAAGAGGGAAAGAGAAAAAGGGGAGAAGG
 AGAAGGAGGAAAAGAAAAGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG
 GAAGGAAGATAAAGAAAGAGAGAGAGACAGACAGACAGAAAGAAAAGACAGAAGACAGAAA
 GAAAGACAGAAAGAAAGAAAGAAAGGAGAGAAAGCAGCTATTTATTTATGGTTGCAATGT
 TCCTGGTGGGGACAGGGAAGAGCCTGAAATGGAACATTACTGATAGAGTCTAGCTCC
 AGGTAAAGGGACCTTCCCCGGGTGGCTGAACAGAAGCAGCTACAGGCAGGTGGAAGTCG
 GAAGTACGCATCACTGAGGGACAGATGGAGACATGAGATCTAGCAGTCTGAGGAGAACTG
 GAGGGCCTGGGGTCCGCTCAGCAAAGGCAGGAGTACCCTGGCCCTACTTGGCCTCTCTGA

FIG. 18C

References

CTCAGAGGTGAGGTGTGATGCTGAGGGTCTGCAGCTGTAAAGTAGGGCGGAGCATGCGGA
GGGAACACTCCAAGTTGTTGACCACCTTCCACTTCCTCCCCAGGGACGCTCTGTGTGGGA
AACTGCTGTGCCAGGGAGGGGAGCCGAACCCACTAGTGCCGCACATAGTGACTATGGACT
CCACAATTCTCCTAGAGGGCCGCGAAGTGGTTTGCCGAGGGGCCCTTGTGCTCCCAGATA
GTCACCTGGACCAGCTTGACTTGGGTCTGGTAGAGCCAGGCACCGGCTGTGGACCTAGAA
TGGTGAGCCCTGCCACCCAACCCCTCCTGGTTATTGAGTCCTCCATGCCAAAGTGTCT
CCTCACTGCCCAGTGGGCACAATGCCCATAGGTGTGCCAGGACAGGCACTGTGAGAATGC
TACCTCCCAGGAGCTGGAACGTTGCTTGACTGCCTGCCATAACGGTGGGGTGAGTAGCCT
AAGGGGTCAGGGTGACCTTGGAGGTCCTTGCTACCTGGTGACTTTTCTATCCTCATCTTA
GGTTTGCAATAGCAATCGTAACTGTCACTGTGCTGCTGGCTGGGCTCCACCCCTTCTGTGA
CAAGCCTGGCTTGGGTGGTAGCGTGGATAGTGGCCCTGCACAGTCTGCAAGTATCCCAAT
GGGGTGGGGGCAGGCAGGAACCACTGGGCAGTAGCCTGCTTGAGACTCAGCACCCCTGC
CCTCCACAGACCGAGATGCCTTCCCTTGGCCATGCTCCTCAGCTTCCTGCTGCCTCTGC
TCCCTTGGGCTTGCCTAGCCTGGTGCTACTACCAGCTCCCAACATTCTTGTATCGAAGG
GACTGTGCTGCAGGAGGGACCCCTATGGAATAGGTAGGTTCCGGTGCTCAGGTCTCTCTT
CCTGAGCCTGCCCCATGGCTCCTGCTTCTCAGAACTCTTCAGGGCTTTGTAGAGTGAGA
GGCTACAGGGAGCTGGGGCTTTAGGAAGCTAGATGGGATCCTTATTCTCTAGATGTAGTG
AGAGCTCCAGGCTGTGGGAAGAAGTCCGTGGTGTGTATCACTGCCCTGACCAGCACTTG
GTGGTGTGGTCCTTTCCATGGGCTTCCCTTGATTTTTTTGTTTTATGTTTTTTGTTGTTG
TTGGTTTTTTCTGCTTTAAAGAAATCAACACAGCCTGTGCTCCGCTTTGTCTGAAGA
CGACTCTAGCTTCCTTGTCTCAATATCAGCCATCTCCCATGGCCTTTGCCCTAATTACTC
CCTTCAGGTCCCTCGGTGCTAGCCAAGGACCCCTTTGTGCTCCCTATAAACTGGCCAGCT
ATAGTGTGCTCTTTCTGTGCCAGGACTCTGTGCCTCTGTCCCCTGTAGATCACAGTGCT
GTAAACCAATTTCTGGCAGGCAGAAATGCCACCTGATAGCACACATTATCTACCGAGG
GCAGCCTCCTCACTAGGCCCCCTCGGGCAAGTCAGGCACATTATGTCCCTGTCTGAACTTG
GAAGTGTCTAGACCAATTGAGGGAAGGGCAGGGTTGGGTTGGAGATGTGACTAGAGGGC
ACCTCAGGCCAGAAACAGCACCCAGCAGGCCCCAGGAGCCAGTGAGACGGTCTGGGGAAAG
CCAGGTAGTGCTGGGGGTGGGGGCGGTGTCTGCAGACAGGAAACAGGTGGAGTGACA
GTTGGGAGGGGGCACTTCAGAGGGGTGGCAGCTGCACACCGTTATCGGGATAGGGTGTC
AGGACAGTGGGAATATCTGGATGAACCATCCAAAGAAATGGCAAGGTCTGTGAGAAAGGT
CCCCGCAGTTCAGAGTCTAGACTGGCAGAGCAGGCTAAACGGAGCATGGGAAGGCACAG
TTCCCACCAAGGGAGACATCTCTGCACTTCAGCTCTAGGTGGGCCCTCGGTGACGCCTAC
ATCTAGACTGAGTGGGGGCTGGAGTGGAGTCACCTCGGGAGAAAGGATGTCCACAGCCCT
GGAGGCCCTGGGACATAAGTGAGGTCTGGACATCTTAAGGACAGAACAGGAATGTGGAAT
TCGAAGCTTGAGTGGAATGGAGAAGCAATCCCCCTTTGTCTCATACACGGTCACTTTCCA
ACCTTCTGAACTCTTATCTGGTCTGTCACTGGCCCCCTGCAGAGACATACCCCTGGGCAGT
GTGCATCCGGTGGAGTTTGGCTCCATCATCACTGGAGAGCCCTCGCCCCCTCGTAAGTGT
GCCCCCTTGGGACATGGAGAGGGAAGCAAGGGGTGGGTGCTTGCCATCTGCCTCCTTCTAA
ATGCTCTCCTTAACACACCTTCAATCCTCTGCCCTGCTCAGCCCCATGGACCTCTTGCCA
ACAGCGTTTCGACCCCTCCATCTCTTGACTTGCTCTCAGACCCTGCGAACTCTGAGCTTAC
CTAAGAACTACCCCTCTGAAGCAGCCTGGTCTACAGATTGAGTTCAGACCTGCCCTATCC
CTATGGTATGGAAGCACCCCTGAGGACCTCCTGTTGCCAGTCACCTACCTCTGTCTCAGT
TTGTTGTCCCTCCTCAGATTTACAGGCTTGCAATCAATAAAGAAATGAGACATGGGCCTC
AGAGAAGCTGTTGTATAGAGACCATGATGCTGGAAGCCCTAGGGGCAGGGAAGGGAGAC
ACTGTGGTCTCTTCTGGGTCTTATAGAGGGAGGACAAATGTGCCCTGCCATGTGACTTG
CAGTCCTCAGTTTCTCAGACGCACTCTTATAATTCTATGGGCTGTATGCTGAGCTCTTA
CTCAGCATAGGAACCCAGAGCCCGATCATGTTGTATCCCGCTGCCCTGAGAGCTGTGC
TATTCTGAAATGTTAGAATGTATCTAATAACAATAAATCCACAAGTTATATCAGTGTGT
TGGCTGTGACCTGTAAAAGGGTCTAAGTTGTTTATTAAGAAAGATATGGAGATGGATTAC
TGAGAAAGAAATTAGAAACAACATCTGGACAGTGGAGGAGCCAGCACTGGGGAGGAAAGG
GCAGACAGATCTCTGAGTTCAAGGCCAGCCTGGTCTACAGATTGAGTTCAGGATAGCTA
GGGCCACACAGAGGAAACCCCTGTTTTGAAACCAACAGTCAAATAATAAAACAACTT
AGTAGCACCTTGACAGACAGAGAGAAAGGTTCCAGGAGAGCTCAGACCCAGCAG
AGGTGGCAAGGCAGAGTCTCAAAGCCAGGTGGGAAAAGTGGGATCTGTTAGCATAAACC
CAAAGGGCGCGTGGGACAGGCAGGGAGTACCCTTTGATGCAAGCTCACTCTGGTGAGGGC
CCCTCACCCCTGGATGTCTGTTAGCAAGGGAATCAGTCAGTGTCTCAGTCTGTTAACATC
TGTGAGAGGGGAAAGGCTGCTGCAGACATGGCCTGAGCAGCATCTGGATTGGAACATTTG

FIG. 18E

CACTTTAGGGCCTGCTCTCTCCCCTGGGTGGGGCACTCGCCATTTCATTGCCTTTACGACA
GCTGTGAGAGAGAGGTTGCTGCAAGTGTGTATGGCTGGGTTAGCTCGAGCCCACCAGGCA
ATCATGATTTCCCTCGACATCTAGTCATTAACAAACACAGGTTCTTTTACTACAATTTTA
ACTACCAATATTAACATAAATGTGTATAAAATATATAACACAGTACACATATATAAGTA
CATAGATGTTAGTACATATAAATATTATATATATATATAAATTGTAATTAATATTACTT
AATTTTATTTTATCATTGATATTATTTTACTGTAGTTATAACAATGTGCATAATATAT
GTGTAATATAAAATATAATTTTATTATTTAATATTATTATATAAAATTTAATTAATATTAA
TTATACCTATATATTTAGTACATATACATAGGTTACAGAATGGCTACAAAAGTGCCAGGA
GCCATCAAGGAGAAGCTAAAAGCCAGCAAGTGATCTTCTGAGACGGTTCTGCCATGGAC
TGTACAATTAGTGATGGATTGCTTCTGTAGGCAAGGACGAGGAGATTTCAATTTAGGAA
AGATTCTGCTATTAATATGCTTTTCTGGTATTATTAAATATATATAACAATCACTAGG
TATTAGCCACCGTTTGAACAGAAATGTTCTGCAGAACAAATGAAGATGTACTCTCTTGTA
ATGATGCTATATAGACAAATAGATTATTTCTTTTAAAAAAGAAAAAGAGCCGGGCGA
TGGTGGCACATGCCTTAAATCCCAGCACTGGGAGGCAGAGGCAGGCAGATTCTGAGTT
CAAGGCCAGCCTGGACTACAGAGTGAGTTCCAGGACAGCCAGGGCTACTCAGAGAACTC
TGTCTTGGAAGAAAAAGAGGAAGAAAGAAAAAGATTTATTTATTTATTTATACAT
ATGAGTACACCATCAGACACACAAGAAGAGGGCACCAGACCCCATACAGATGGTTGTGA
GCCACCATGTGGTTGCTGGGAATTGAACCTCAGGACCTCTGGAAGAACAGTTGGTGCTCTT
AACCCCTGAGCCATCTCTCCAGCCCAATAGATGATTTCTTAATTCTTAAGGATGATCCT
ATAAGAATTCCTAACTTACATTAGTAATTATTAAGCTCTTTTACAATAGGACTTCTATT
AAGTCTTCTCTAATATGAAAACCTCAATAAGAACTCTGCCAGTCTCAAGTGTCTAGT
TAGTGTCTTCTGAGATAGCAAGTAGGCATCAACAACCTAGAGCACATTCTAGGAGGTTGT
AAAACCATTAACCAAGTGGTCTTAAAAAGGGAACATAACAATAGGCTATAGGTGCAAGGACA
GAAGATAAAATATTGACTAGGTTTATCAATACAAAATTTACCCACAAAAGTTATGTTTTT
GACTTTTTCATAAAAACCTCTTTATGAACCTGTAGAAGTGGTGAAGATGACGAATGCTTAG
CCAGATAATTACTCCTAATAGATATGCATGTGAATATTCTGTGCTGTAAACTTATTTATG
TTTGAACCTCCAGTGAACCTTTTGTTTAAAAAGGGGGGGGGTTGAAAAGCCATGTGATC
TATTCTCTAGAAAAGGTTACAGAAGACTAAGAAAGATTACATTGGAGATGTAACCTTGGGA
GAGAAAGCTTTGGGAGCAAGAGCATAGAGAGCAAGGCCATTGTGGCATCAGAGCAGGAGG
AGAGAGCAAGATTAGAAGGAGATGCAGAGTGGAACTAGAACTATAAGGCAACATA
AAAAATTAAGAGAGCCATATGCAGAATGCAGAGGGAAAGAGAAAAAAGAAAAAAGA
AGCTGCAGGGAGAGCAGAAGGAGCAGGCAGGCTTCTCTGACCATGGGGTAGAACAGGGC
TTTTCTTAATACCAAGGCAGGCTTAGTCTTAAGGATAATAAAGCTTTTCTTTCTTACAGA
CTTGGTTTTAATTCATTTAGCAATAAAAGTGTAAGAGTGTCTTTCTTCCCTATGCAATAA
AGATTGGAGCTTATTTTTCAGCCAGAATGAGTGAGTTCTCTCTGCAACGGTCTGGTCT
TTTGTCTTACATACACACATAAGTGTGTGTGTGTGCGCGCATGCGTGTGTGTGTGTGT
GTGTGTGTGTGTGAAGTGTGCAATTATCAGATGGCATGGAAGCTGGGCTCAATTGGTTC
AAATGGGGACTTGTGAGGGTATATGCATGAATCTGTATATGAATTCATGTGAGCTTATAT
ATATTGCTTGTGTAAAAGTTTTCTTCTGTGTGAGTGTGACTCTTCTCTCTGGTTCAAT
AGAGGTTTATTGCTTCAAACCTTCCCCCTAGCCTGACAGTGCAGAGGCATCTGGACAAGAG
AGAAAAGGCTCTAGCCATTAATCCTTTTCTTAGATCCATTTTCTTAGAGAACTTCTTAG
GAACTGTTTAGAGAGAACATAGAAAACAGGCTGAAATCACTTGTCAACTGTCCCCTTTT
CTTCTTAAGGACTTCTACTAGCAGACTGGGAGTTAGAGCTGCACAGTCCCTGAGGAGATA
GAACAAAGGCTGCTTTACTGAATCCCCCTGCTGTTTTAAGATGAGGTTCTAAAGGAGATTG
CAGTTTCTGACCCCCAAAAGGAACCTCAGGCAGGTCAGCTACAGTATCAAAGTGACTTAA
CTTAAGATAGGGATATGTTTTATTATTAAACAGCTACCCTAAATATCTCATAAGATCAAG
CTTACCCCGGTGACACTTCCCCCTCTGTTGCCTCAAGAGGAACCAAGCAGAAAGAACCGC
CAGGGCTGGCTCCTGGCACAAATGGGTTAAAGATGTTGTAGCATGGGGAAATGAAGAGAT
GGCTCAGCTATTAAGAGAATATCTTACTCTTCCAGAGGACCAGTGTCAATTCACAGCAA
ACATATCAGGTGCCACACCATCACTTGTAGCTCCAGCTGCAGATCTGCTACATCTGGCCT
CCATAGGCACCCACACACAGGTGGCACCACAAATAAAAAATAAGATAAATCTAAACA
GCAAGTTAAAGCATGAGCTGAACTAGTAAAGTGCTTGTGTGGCATAGACCAAGACCTG
GGTTTGGTCCCTACCTGTTAGAAATAGTCTCAGTATCACACAAAGGAACACCAAGCGAA
GCAAAAGCTCCAGCAAGACAAAACCTACAGTCTTCATTGAGAGTGTGCACGCTGAAGACC
GAGCACACTGGGTGCAAAATGTACTTGGATTCTGTTTGTCTGTTTTGTCTCCAGACAGGGT
TTCTCTGCATAACAGCCTTGGCTGTCCCTGAAATTCAGTGTGTAGACCAGGCTGGCCTCA
AACCTCAGAGATCCGTTACCCACGCTTATCTAGGCTTCAGTCTCACCCTGTGAGATGG

FIG. 18F

CCTGAAAGTTGTTAGAACCGCGCGGGATCTATTTCTGACAGACTGGCTGGCATCTTTTCC
TTCTCTCAGCATGAGATTCTTGGGGCGTTCCCATTTTCTGACATCAAGCATGGTAGCAGAGT
TGGAACCTGAGGGCTGAGGGCTCAGACTCAGACCATAAACTGGAAGCAGAGAGAACTGGA
GATTGTGGGAGGCTTTGAAACCTCAGCTCCTGCCCCAGCAAATACCTTCCAGCAAGGCCA
CACCTCTTAAACCTCCCCAAACAGGGTCACCAACTGGGGACCTAATATTCAAATGCCAC
AAATATGGGAGACATGACATCCAAACCGCCAGGACAGGTGTATACCTCCATGCTTGGTTT
CCGTAGTAAGAAACACTAAACATTAGCCTTTTCTTAATAAACACTGATATAAAGCCCTGCT
ATTCTCGATGTTTTTCTCTGTCTGCTCCTCTCTCCACCTGCTTCTGTCTCTGA
CCTCTTCTGTGTACAGATAGCCCTGCCATGTCCATCTGCCAGCCATGTTCTGTCTACTT
GCCTCTCTCTGTCTGTGACTCTTCTAGATGCCTCTGGCTGTTCTTTCTCATATCTACA
ATAAAAACCTGGCCCTTAATCATACCACAGAGATATCGAGTCTTCTTTATACAAATTTTC
TTGTAGCTCTCTTAAAGGGAGATTAAATAAACAGGCTGAGCACACAGGAGGATCATGGCA
TATTGACTTGCTTGTGAGGTTTCTGAGATGTTTCTGAGGCTCTTGAATGAAAGAGATCTTT
CATAAAATTTCTATACAGACAACAGCTAAAGACTTGATGGGAAAATACTGGTGAGTA
GGCCATGTCCAGGTTACTAATAGCCTCTGCACAGGGAGAGCCCACTGTGGAGAATAGGC
CAAGGACAGGCCGATAATCGCCTTATTTAGATCTGTTCTTTAAGATGTGTGTGTGTGT
GT
AGCTGTCTTCAGACACACAGAAGAGGGGCATCACACCCCATACAGATGGTTGTGAGCCAC
CACATGGTTGCTGAGAATTGAACTCAGGACCTCTGGAAGAACAGTTAGCTCTTAACCATT
GTACCATCTCTTCAGCCCTTCTTATATTTGTATTTTAAATAGCTTAAAAAGAAAAAGA
AACCATGAATGTGAAATTAGCATAAACTTTAGTGTTCAGAAATAGATTTTTTTTGGAAC
ACAGCCAGGTTCTTTCTTGTGTTGACTGTGTGAGGGCATTCTGGGAAACAGGGTGTGGCC
TGGGAAGCTGTGAAGGTGTACTTCTAGTTCCTTCTGGCCCTCCTGCAGACAGTGCAAGCC
CCACAGTACACTGCTGCATGTCTGGGGAGGTTGTTCCAGCTGCTGAACAAGTTCTTGTGG
AACACTGTCACCCCTGCCCTGGGGTCTAATCATGACACTGCTGCTCCTCAATGTTTGAAG
GAAAAACACCCCTTAGTCTCAATGCTGTATAAATAAACCCCTCTATAAAATCAAAGGCCGC
ATTCCATAGGATGAAACACGCGGGGAACATTTTCTTCCATGCCAGGCCTTCTCTTCTG
GCAGGGCTCCAACATGTCTGGTCTGCCTGCCCTGACGCCAGGCTACGGCTGGCTGACTC
CTTATCAGGCACGTAGCCCTCCTTGGTCTGTTCTACCAGTCCCCAAGCCTAGTCCAG
GTCAATGCACAGATTGACCCCTGTAATAGTAATCTTGGGGAGGGGGCGTTCTATGTCC
CTTTTTGCTCCCAAATAACTGCAGAGTGTCTTATACCCACTCGAGCCGTAAAGATACAG
AGACCTGGCATTTTTATTAACAAGCTATTAGAGTGTGTAATATCCGGGCAGATTC
TTATCTATCCTAACCCAATTAGACTACCTACTACCCAACCAAATGCCCTGGTACTTGCCC
TCTGGTCTTGCCCTGCTTCACTCTGGTCTATGTATGTTCTCATGGCTGTTTTCTCATGGC
GAATCTTCTGGTCTCTCCACGTGGTTTTCTCCACACCGTCTCCTCCTCCTGGTCTTATC
TACTCTCTGGTCTCCTTTGGGACCCCATGACTGGGATTGGAAGTCCCTCCCTATCTCTC
TGCTCAGCTAATTGGCTGACCAGCTCTTTTATTAACCAATCAGAGGTGATGGAAAACAAT
GTTTACACAACATTGAGATCGGGAGATGGCTATCTTCCAGACTGCAACCAGATGTCTGCG
GTAAAGAAGTCAGCATCTGAACAACAGTGCACAAAACCATCCCCAACAGCCCACTCTG
GCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCT
GAGAGTTTGGTTTCCAGCAACCAGCCTTCCGAGAGCTGGTGGCCTTCTCTGGCCTCGGGG
TAACATGCATACATGCCCCATAAAATCTGCTTTACAATGCTGTCTTAATCTGACCAGAAG
AAAAATGTAAGACTAACTCAGTAGAAATAGTCCAGGAAATAACTAGTGAGAATTCTTATGA
AAAAATGGGGATAAGGTGAAGGAGAGTTTAAACATCCAGGGGAAGTTGGGACGGGCTTCTC

FIG. 18G

>Mouse 216 homologue aa sequence

MGSRCGRPGGSPVLLLLPLLLLPSCPLRSARMFPASIPKPHLHIPTCTWLTNYEAHVTLRT
RFELELLLFQILKMYMSVLPAAHASVYRGGNAHGEIVTPHWILEGRLWLKVTLEEPILKPDS
VLVALEAEGQDLLLELEKKKKLLAPGYTETHYRPDGHVVLSPNHTDHCQYHGRVRFRE
SWVVLSTCSGMSGLIVLSSKVSYYLQPRTPGDTKDFPTHEIFRMEQLFTWRGVQRDKNSQ
YKAGMASLPHVPQSRVRREARRSPRYLELYIVADHTLVSPSDSQDSGYTVGVDRAGSVDR
AGSQSHHSGRKRNALGFPTVAPRGVGQETTRLHTTAHDHSELPIGTAATMAHEIGHSLGL
HHDPEGCCVQADAEQGGCVMEAATGHPFPRVFSACSRRLRTFFRKGGGPCLSNTPAPGL
LVLPSRCNGFLEAGEECDGSGQLKSAGTPCRPAATDCDLPEFCTGTSPYCPADVYLLD
GSPCAEGRGYCLDGWCPTLEQQCQQLWGPGSKPAPEPCFQQMNSMGNSQGNCGQDHKGSF
LPCAQRDALCGKLLCQGGEPNPLVPHIVTMDSTILLEGREVVCRGAFVLPDSHLDQLDLG
LVEPGTGCGPRMPHGPLANVRTLHLLTCSQTLRTLSPKNYPLKQPLQIEFQTCPIPM
REDKCALPCDLQSSVSQTHSYNSYGLYAELLLSIGTPEPDHVVSRLP

FIG. 19

>Gene 216 genomic DNA sequence

CCAAAAGCGAACACACCCAGATCAAGAAATAGACCATCCTACAGTCCCCCCTTACACTCT
GTACCAGTTGTCAGCCCCCACAAGGGTAACTACTGTCTTGACTTCGAACACCATAGATTTG
ATTTGCCTGTTTTTAACTTTACATAAGTAGAATCACAGAGTGTGTACAATGACTTTGGA
AACTGTTTGACAATATCTATTAAAGCTAAAATACCCTTGCCCTATGAACCTGAAATTCC
ACCCACCTTGCCAAGGGACAAAAAGTTCCCCTCTAAATGCACCAGGCTGTCAGGGATGAA
GCGTTGGCTTTGGGGCCCCCATTACACACATGACCTTTTCTGGGGCACCCAAGCATCAG
CCTGTCGTCAACAGGTGCCACCCTGGCGATCTCTGAAGGCTGGAGTCGGAGTGCCTCCCT
CAGACATCCTGTTCTGCGTCACTCCTTGGGAGAAGTCGTGTTTACAGATGGTGGGTGTCA
CCCATGCCAAGCACTTCTAAGGGTTAATGCTCACTGGTTTGCCTGGTTCCCAGGACATTT
CCTGATGCCCCCTCTGGAGGGTGACGCCAACAGCCAGTGGAGAAGCCATCTTTCCCAGGT
GCTGTCAGGCGCCCCCGGAGCTGCTCGGTGCATCCTAGGATCCCTCTTCTCAGCTTTGG
TTTGATGGCCTCATCTCCTCCCCTGCAACCTCAAATGTAAATAAACCCCTTTCTCAGAGA
CTTCGGCAGAAAATTCCTCTGACCTGCACCTGGACACAGCTCATCTGGGTTTGGGAGGTG
TCAACTGTGTAAAGTAGTCTGATCCCCATGTGGCTTTTCGACTGTGTCCCCTCTACAG
TCAGTTATTAGCACTGACTGTGCTAGGAAGTGAGCAACACACATATTCCAGACCACATG
GAGCTCAGGAGCTTGGGGAGAGAGACAGGGAAGTGGACGACTACAGGGCCTTCTGAAACG
TGTTGCAGGGAGAAGTGTGAGTCAGGCGATGCTAACCTGGCTTTGGGTAAGGGACAGCCT
CTGAATGACAGGACATTAAAGCCATGGCCTGCAGTTTAAAGTAGGAGTTGGCCAGTTTCGAG
GTAAGAATAACAGTAAGCAAGAACGCCAGAGTAGCTCCTCGAGCTGCCTTCTGTACCTGA
CATCCACACTGAAGCCAGCCCCCTCTGTGTTTCAGCCTTGCTTTACTGAAGAGGTGTGCTG
AGGGGCTGCTCTGGGGTGCTGCTCTGCTTTCTGTCCCCAACTTGTTCTGAGCTCGAGCC
ACCTCCATACTGGTGCTCCTGGTTCTCAGGCCTTTGAACTCAAAGTGAATCACACCCTG
GCTTTCTCGTTCTCCAGCTTGAGATGGCAGATTGCGGAACTTTTTGGCCTCCATAATC
ACGTGAGCCAATTGCTATAATAATATCTCTCTCCCTCTTTCTTCTCTCTCTCTCTCTG
TGCAAATATAGTTCCAATTATAAGAGCCCCCTAACTGGAAAATAACCCCTATGGTGCACTGG
TGAGTAGAGAACTGTGGTTCCCTCAAACCACCGAACACTATTCAGCAATACGAAGGAAC
AACTATTGATATGCAAATAGTGTAAATGAATCTCAAAAACATCGGAAAGAGGGAAGGA
AGCCAGACACAGAAGAGTGCATGCCGCATGATTCCATTTATATGAAATTCTAGAACAGGC
AAAACCTTATCTATAGACAGAGAACAACAGATCAGTGGCTGTCTGGGGTTGGGAGTGGGGA
AGTTTGGCTGGAAGGGCACAGGGCTCTTTCTGTGAGTGAGGGAATGTGTCTGCATTATAG
TGATGCTTATGTAGTTATATACACTTATCGAAACTCATCTTACTGGCCACTTAAAATAAG
TGCATTTTATTGTGTGTAAATTATACCTTAATGAAGTTGATTTGAAAATCCAAAGTAGTA
ATAATAAGTAATAATCTCGTAGCTGGACAGCTGTGGTGAATCACTCCTGTAATTCCAGCG
ATTTGAGAAGCTGAGGCAGGAGGATCACTTAAGATCAGGAGTTCTTTTTATTTTTATTTT
TATTTTTTTGAGACGGAGTTTCGCTCTTGTGCCCAGGCTGGAGTGCAATGGCATGATCTC
GGCTCGCTGCAACCTCCACCTTCTGAGTTCAAGCGATTTTCTGCTCAGCCTCCCAAGT
AGCTGGAACCTACAGGCGCTCACCACCTGACCGGCTAATTTTTGTATTTTTTAGTAGAGAT
GGGTTTTACCATGTTGGCCAGACTGGTCTTGAACCTCCTGACCTCCAGTGATCTGCCCCG
CTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGACACTGCGCCTGGCCAAGACCAGG
AGTTTGAGACCAGCCTGGGAAACAAAGTGAGACCCCTGTCTACAGAAAAATTAAAAATT
TTAGCTGGGCCTGGTGCCGTGTGCCTGTAGTTCCAGCTACTCAGGAGGCTGAGGTGGGAG
GATACCTTGAGCCAGGATTTCAAGGCTGCAATGAGGCATGATCAGGCCACTGTCCTCTA
GCGTGGGTGACAGAGTGAGACCTGTCTCTAAATAATAATCATAAGAAACAACAAGGACCC
TCTAAACGCACTGATATCTAAGGTGTATTAAGCGACCAAAAAAAAAAAGAAATCAAAGT
GCAGAAAAACGTTAATAAGAGAAAAAATATGTCTGTATTGTCTTGAGTGTGAAAAATA
ATCTAAAAGCCTATGAAAGAACTAATCATATTGGTTTCTGTTGGTGAGGAGGGCTAAG
AGCACGGAGACTTTTCCCTATGCTTTCTGTACTTTTTGATTTTGAGATATGTGAATGTAG
GTTTCTCTCACTGCTCGAAGTTTCACTAACCATAATTACTACATTCCAAATTCTCAAAAC
AATAGATTTACTTAAAAGTAGGCTGGGTGCGGTGTCTCACGCCTGTAAATTCAGCGCTT
TGGGAGGCCGAGGCGGCAGATCACCTGAGGTGCGGAGTTTCGAGACCAGCCTGACCAACA
TGGAGAAACCCCATCTCTACTAAAAATACAAATTAGCCAGGCGTGGTGGCGAATGCCTG

FIG. 20A

TAATGCCAGCTACTCGGGAGGCTGAGGCAGAAGAATCACTTGAATCTGGGAGGCAGAGGT
TGCAGTGAGCCCAGATCATGCCATTGCACTCCAGTCTGGGTAAACAAGAGAGAACTCTGT
CTCAAAAAAAAAAAAAAAAAAAGATTTGCTTAAAAGTTAACATCTCCGGCCGGGCGCG
GTGGCTCATGCCTGTAATCCAGCGCTTTGAGAGGCCGAGGCGGGTGGATCACGAGATCA
GGAGATTGAGACCATCCTGGCCAAAATGGTGAACCTCGTCTCTGCTAAAAATACAAAAG
TTAGCTGGGGTGGTAGCGCGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAG
AATCGCTTGAACCAGGGAGTCCGAGGTTGCAGTGAGCCAAGATCGCGCCGCTGCACTCCA
GCCTGGCGACAGAGGGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGTTAACATCTC
ATCCAAATTTGCACCGAGTAGGAAAACAAAAGTTTAAACATGAAACAGATGTTACTGAG
GCCGAAAGGGTCTCCCAGGCCTGGGAGTCTGCAGCTTTTATGCAATTCTGCCCTCTGGCC
ACCGCCAGGGAAGAAAGGTTGTCTCCGTCTGCTGCATCGCCTTTGCCCAGCAATGAAGCC
CCCAAGACAGCGGCAGCCGTTGCCTGAACCTTCTATCCTTGGGGGCACCCAGTGCAGG
TGGATGACCCGACTCAACCTCCGCCAGGGCACCTCGGGGCAGGACGGGTAGCAAGGAGG
GGACAGAGATCGGCCCCAGGAGACCAGGAAGATCGCGCTCCTGGGGCCAACCTTCAGCAG
CGAGAGGCGGCCTTTGCCACCGCCTCATCCACCACGCGCGGTCTCCAAGAACCTTC
CCAGCGGTTCTCTCCTCCTCTCAGGAGTAGAGGCCCTCTGAGACCGACGGGGAGGGACGG
CTCGGGCCGGTTCATCCGAGGGGCGCACGGATTCCCTCCTCCGCCAGCTCCACCCCTC
GAGGGGCGGCGGTCCGGGAGTGGCGACCCGGCTCCCCCATGGCGCGCGCCGTCTGGGGCCC
CTGGCCAGGCTCCGAGCGGGGTTGGCGGGGAGGGGAGGCGGGAGCGAGGGCGGGCGGTGG
GAGGTGGGGGCGGGAAGGTCCGAAGGCGGCGGCTGAGGCTGCACCGGGCACGGGTCTGGC
CGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCA
CAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTAC
TGCTGCTGCTCTGGCCAGTGCCAGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGC
TCCGCCCTGAGGGGCAGGCTAGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGC
TGCGGCTCAGCGCGCGGAGGGTCTCACGGCCCCGGCACCATACGGCCAGTAGGTACGGGCG
TGGGGACTCTTTGGGGGGGTCTCCGTGGGACCTGCCAGGGACGCTCAAGTGTGCTTGGG
CTGGCCCCGGGCCCCGACTTGCCACACTGCCCGGTGCCACTCCGCTGGCAAAGCAGAG
GGCATGGCTCCCTCCCCCTCGGGGACAGCCAGCCCCAGCCCCAGCCCATAGCCGTAG
CCCCCTCTGCCTGGATTCTCGCTCTACAACCAGCTTCCATCCGCAGGCCACCGTGTGAC
CCGCTCCTGCTCCTCCACCCCTTAGGACTCAGCGGGGCTCCATCCTCTAGGAAGCCCCCA
TGCCCAAGAGTCCCCCAGAGTCCCTGCTTTGCTCTCAGGCTGCAGAACTAGCTGTGGCCT
CCACCCTGCTCACCCCTCGTCCCTCCTCCAGGGCAGCAGGGCAGTGTGTATGTTGTTTA
TATTGTTGCCTTGTTTGGTGAAGATAGAGAAGGGCCTCTCCAGATAGAAGGTGCTGTTTA
GCAGTGCTCTGGAAGACTGCAGCTGTCTCCTCGGGGTAAACCCTCCAAACAAAGATGTT
AAGATGGGGCTGGAACAACCTCTGCAAGCGGGTGGGAGGATTAGCCAGTCTGTCACAGCA
AGTGCCCTGGCCGGGAACAGGGAGGGCAACCAGGGAGGGGGCATGCGGGGCTGGGCTGTGC
TATGCAGACTGGGCGGTGGCTTCCACAGCACTGTGTGGGGACCAACAGGTACAGGGGCC
TGGTCTGTTCTGGCCCCAGGGGAGGGCCCCAGGCGGTCCACTGCTCCCTCCCCTCTGAGC
CCTATCCTGGGGTCAAGGGAGGTGATGGGACCCCTGGGAGAGGGGCGTCTATGTGCCCAA
TACCAGCCTGGCTCCCTCGGGTTCCACCCCCATTACCCGGTACCCGGAGCTCCAGCTCC
AGCTCCAGCTCTGCCCCCTCTCTCCCTCATTGGGGTCAAGGTGCCCGTGGCCAGCACGTGC
GCGCAAGGCCATGTGGACAGCACCCACACACACTGCACCCACACCACACCTGTGCCC
GGGCCCCACCTACCTCTTCCCCAAACCCTTAGAGGCCTAGGAGCAGCAAAGCTTGGTTCT
CTACTCTCAGTTAAGTGCTCTCTGGGCTGAGAGCCTCCCCTCCTTCCCCTCCCCACAT
CCACTCAGAGCCCTCCCTGCACTGGCCCCCTTAGCCTCCTTTCCAAGGTGGCAGACTCCT
CTCGGCCCTCATCTGCCTGATGGCAATTCATCATCCAATCAAGGAGGGCTTCTTGAGG
AAGGCTCTTTGATGTTTGTAGTCTGGGAGAGAAGGTGGAGGAGAAAAAGGAGTTGGGGT
GGCCTAGCAGGAGCTGAGTCACTTCCACAGGCAGCCATCAGCCAGCAGGACTGAGGCCA
GGGCTGCGTGGAGGGGGGAGGCTGTCTGTTCTGGGAGCTGGGACTGGGTACCGGGGAAG
GAGGGCTGCTGCAGGCTCTGGGTGCCTGGGGCTGGCTCCTGCAGGGCGGGCCTGTGAGA
GTGTTGGGGCCAGTGGAGGGGCTGGGAGCATTCAGGGGAACATTCCAGGGCGCCCTCTG

FIG. 20B

AGTAATGCTTGGCTCTGGGATTCCTCCTAGAGCCCCCTTAGGCACACCCGGCCAGGGAGC
ACCAAGGCTCCGTCCGGAAGCGTCCCCCTCCCCCTTGAAGAGATGAGGAGGGGCCTTCTGGG
CCAGGGTACCAAAACCTGCCACCAGGACAGAGTCCCCGAGGGAGCTCTGGGCAAGGTGG
ACCTCGCAAGGCAACATCTGGCTGTTGTTTTTCTCAGATGATGGGGGGGGCACAAGTGTC
CTCTCTTCGTACATCTCTCACCCCTAAAGGCATCTGCTGCCCATCTAAAAATCCCTAAGGC
TGCCGCGCTCTTTCCTTCCCCCTCTGCACTGGCGGCCTTGGCCTCTTCCTTGTGATCGCCG
AGCCCAAGCCTGCCCCCGACAAAGGTGAGGGGACTCCCGTGTCCCCAGCTGAGCTGTCC
CTTTCAGCCTTCTCTTTTCTCCTCCTTGATAGCTCCTCAGATCCAAGGATGCCACGG
GCGTCCCTCCTTCTCCAGGCTGAGCCACGCGTGTGAAGGTGAAGTCTGCCCCAAAAGG
CCTCCAGTGCCCTCCCTGGGGATGTCTCTACCCCCCTCCCTCTGCTTTGTCCCATGCCCC
TGTGTTCTCAGGTCCCCCTCACCCCTGTGCTCTGTCTTTACTCCAGGACATATCCCTGGG
CAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAG
GAGCCGGTCAGTGCCATGTCTCCCCGCCCTCCACAGGGGCCCTGAACCTCCAGCCCTTT
TGTCTCTCCCTACATTACAGCTTCTAGTTTTGCTGGGGTCCCCAGAACCACCAAGTCACT
ACTCCTATAGGCCCCCTGCCTCCCCCTGCCCCCTCAAGTGGGCAGAAGAAGGCACTGGGGTTT
GGACATCTGGATCTCGTGAGCCCGCACACATGGAAGTCATTTAGCTTTCTCCACCCAC
CTCCCTCTTTCCCTCCCTCCCTGGATGATCTGGGCCACCCCAACCCCAAGGACAGAAA
TGGGTCCAGAGTTTGTGGGTCTGAGAGCTTTTCAGGAGCCTCTAAAAAAGGAGGAGGAG
AAAAAGCACCAAAAGAAACCTTTTGCAAAGTTGACCAGAACATGTGACCCTGTGGACA
CACTGCTGTCCCTCTCAGGGCCCTGCCACGAAGGCCTGAACCTTCAGCCTCACTGGCTCC
TGTGGAATCCACTTCTGGTATGGGGGGGGCAGTGGTCACTCTCCTGATGTCCCCCAGATG
TAAGACCACCCCATGTGCTTCTTCTGCAGGACGCTCTGCCCCAGCCTCTTCCCAATCCCG
CTCTTCACACGCTTCCAGAATAACCATGCCCATCTGTTTGTGCCATAATATCTGTGCTG
CAAATAAGAGGGGCAGTAGCCTTGATATGCTCATTTTACAGAGGGGCAAACGGAAGCCCA
GAGAGCTTGGGGAAATTGTCCATGGTCACACAGCTCTTTAGGCTGGGAGCCTGAGACCCA
CTAAGGTCTGAACGATTTTAAACCATTTGGCTACACCCCTGCCCCCTCCTAGAGAGCCCTCT
TTGTTTGAATTTTTCAGCCCTACTGTCCAAATCCAGCAAGAGGGAAGGCAGGGGAGCATT
GCCATGAAGGTGAGAGGCCCCCAGAGACCCAGCAGCTCCCAACCCAGGGCCCTCACTGG
GATCCCCCTAGGCCATAAGGCCCCCCATTCCAGTGTCAAGCACGGCACTGGCCTGAGCTT
TGAGATTGCCCTCCCCATCCCCAGGAGGGGAAGGCTGGACACACACTGGGGTCACTCTGC
CTCTGGGCCTCCCTGTCTGTCTGGCCTGGGCTGTGACCAAGAGGAGAGCCCCAAAGGGGC
TCTGCTTCCCCACCCGGTGGGCCCCCTGCCCCCAGGAAGCCTGCCAAGATGGTACAGAAGA
AAGAGTAGAGGCTAGGTATCCCCCTCCAAAGGCAGGAAACACTCACATTTCAAGATGAGG
GGTATATATCAAGGGGCAGGGTACCAGGAGGGCAAGAGTAAAGATAGCAGGGGCTGCAGA
GGAACAGGGACCTCGAGTATGGCCTTTTTCCCGGTGCAGACCTTTCCCCAATAAAGCAAG
TGGCATTCCAGCCTCATGAGCTCATGCTGGAGGCCTTGTGGGGCCTGTGGCCAGGGAGGC
AAGGACCATCTGCTCCCCACTTGCGAAGGAAGAACTCCCTCCAAAGACTCTGAGACCCTT
GGACAGGGCCCCCAGGCCAGTGCATTTTTGGAGAAAAGGAGTCGGGGGTAAACATTCCGA
AGGCGCAGCAGCCTCCCAGGAAGCTCCTGGGCCGGCTCCAACCTCTGGGCCCCAGGCCAG
CTGAGTGGACAAGGGGGAAGTGGGGTGTTCACACAGGGTGGGAGACGCCAAGAGGGTGGG
GGAAGGAGAGAGGGCTGGCCGTCCAAGCCAGCCTCCTGACACCTAGCTGAGAGCCAGTGT
GCTCTCTTGGCTGGAATGGCGTCCATGTTTACTTCGTGGGTCCAGTGAAGCAGGTGTGCG
AGCCGGAGGGACGGGGGCTGCTGGAGGCCCAGGAAAACCTTTGGAAGAGGGAGCAGTTTGC
CAAAATTGGAAGTGGAGGAGTCAAATTTGAATTCTATAGGAAATGAGCAGCAGCTCATTT
GGAACCAAGCCTCAGGTAGCAGAGGCTCTGAGGAGGCCCTGACCATGGCTACCCGATGCC
CCCATAAATGTCCTCAGCACCCCTCTGTCTTCCCCTGCTTTTGTATGCCCTTCTGGGCATG
AAAGAAGAGGGCGGGGCCAGGGGAGGGGCACCTTTCTGGGACCTCTGGTCTCTAGGGAGG
ATGCTGGTGTGCTGGCAGGCTGTGCCAACGCCCTTCCAAGTGGCTGTTGTGTCAGGACTGC
AAACATCTGAGTTTGGGAACATCTTGTATGTTCTCACCTCCTCCACGCCCTCCATAGT
ATGTGGGGGCTCTGCTGACTCCCCAGCCACGTTCTCCCCAAGAACTTCTCCCCAGCC
GGCTCCACAGGCCACCTACTCCCTGGCAGGCAGGAGGCCTGGAGGCCACCATCTCAGCTC
CACACTCTTTCTTGCCAGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGA

FIG. 20C

AGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCAGTGAGTGCCAGGCTGGGGTAGGGC
TGGGAGGAGGGGATCAGTGTTGGGGGGCAGGGACTGACACAGATCTGTGCGGGTGGCTGG
ATGGGCAGAGGACCCAGAGAGGGTGCAGATGACAGGGAGAGTCACGCAGGCCTGTGGTT
GGCTCCCTGGAGGCTGAAGAGGACCGCTGAGGCTGTGAGCCCCGCTGTGGGGCACCTCCG
CCCTCCCAACCCAGGAGCGGCTTGTTAGCTCCCTGCTGGCGATGAGTGAGCACCACTA
GTGGACATTTGCAAGATATGCTGAGTCTAAAGAAATCCTAGAGGGAAAAGATGAGCCGGC
ACCCAGGCTAAGGGAATGGCAGGGACCAAGATGCGGTGGCTTTGGGAGGCCGAGGCGGG
CGGCTCACCTGAGGTGAGGAGTTGAGACCAGCCTTGCCAACATGGTGAAACCCCGTCTC
TACTAAAATAACAAAAATTAGCCAGGCGTGGTGGCGGCGCCTGTAATCCCAGCTACTTA
GGGGGCTGAGACGGGAGAATCGCTTGAACCCCGAGGTTAGAGTTGTGGTGAGCCAAGAT
CACACCACTGCACCACTCCGGCCTGGGCAAAGAGTGAGACTCCGTCTCAAAAAAGAGAA
AAAAAAGAAAAAGAAAAAAGAAAAAGAAAAAGAAAAAGATGCAGTGGCTAC
ACTTGGGGGAGCAGGTTTGTCTGACCTGCCTGGAAGGTCTCCATCTACAGGGAGGGGAGC
AGGGGGGAATGAATTTGGAGAGTCCCAGGAGGGCCAGATCACAGAAGGCCATTTTGGTGC
TCAGTGTCCTGGACCATCCAGAGCCAAAGATTTTGAGCTGGGGAAGGGACAGGCAGACCT
GTGCTCAGGAAGGTGCCTTGGGCTGGGTGGGGTGGGTGTCCGGGCTGGAGCGCAGGCTCT
TAAAACCACCCAGATTATGTTATCAGTATATATCACCTACTGAGTGCTTGACCGCAGGCG
CTGTTCTGAGCACTTGACACGTATTTTATTCTCCCTCGTGGAGTCGGATGGACAGGGAAC
AAACTCTAGTTCCTACTGTGCCCAACCATATTTTCCCGACGTCCCTACCCTTTCAATGGGG
TGGTCACATCACCTACCTCCTAGGGTGGCGGGTGTGTGTGGGGCAGGGGTAGGGGGCAGA
GCTGGGGCAGGTGGTGGAATGCCTGGGAGGGGGGAAGCAGCCATCATTAGCGGGTGGTCT
GGAGGTAATGAGGCCAAGGTGAGGTGGGTAAAGGATTTTCTTTAAAGAAGACAGATTGA
CTTATGATTGATCCATCCGTGTGGGAAAGATCCTGTTGAGATGGAGCCTGAAGATGGAAT
CATTACCGGAGTGGGTGTGGAGAAGGCAGGGAGGGTGGGAAGCAGCGTGGGCAGGTGGCGA
TTCTGTTTTCTCTGGAGGCAGGGGGTGGAGCATCAATCACTGAAGGACAGGTGGGAGGTAT
GTGGGGTCTAGAAGTCTGAGGAAAATATTTCAAGGATCTAGGGCAGGTGGGGGCAAGAGG
GTCGACCAGATGCCCAACAAAGGAGGGCAGCAGGCAGGGGAAGTGGGGGAGGTCAACGCA
TTTCCCCAACTCCAAGTCCCATTTCTTCGGCAGTGTCTCCTGACTCCTCCCCCTCCCGATCC
TGTGGATCCTGCTGCCTGCTGCAGGTCCCCTGGGAACCAAACTCTTCCCCTATTCCCA
CTCCTCCCCGGCGTCCCTCCCTGGTGCTTCCCATATTCACATCTCCCACAACCTAAGCCATC
ACCAAGGCTCCTTCTCTAGCCCCAAGAGTTTCTGATCTGAGCAAGTCACCATTGCTCCT
GTCCCTTCCCTAAGACACACTGTGAGTGTCTCACTATAAAGCTGCTCCATTAGCATTGA
GGGAGGAAGGCTGGGAGACATCCTGGAGGAGGCAGGAGGAAGCTGAATTCAGTGTTCCTT
GTAACACCCCTCTCAGCAGGCTGTGGCCCCCAGGATACATAGAAACCCACTACGGCCCCA
GATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGTGAGATGCTTCCATGGGCTCTGG
GATGCACCGCCAGAGGTACCCCCCACCATTCTACCCCTACTCCTCCTTGCAATTCCTAA
GGGGCGGTGGAGCCAGCCCCCTACCACACCCTCCCTCTTGCCCCCTCTTGCTCCAGCCCTG
GCTGAGATTTGGGGCTGGCCCCCTTCTCCCTAGGATCATTGCCACTACCAAGGGCGAGTA
AGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGGTGAGCTCTG
GGAGAGGAGGCTGGGCCTGGGATGGGGAAAGAGCTCCCTCACACCCGCTCCTACCCCTCT
GCACCCTAGTGCCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCC
ACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCAC
CTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCCTTC
TGGTGGTCCCCAGAGCAGGGTCAGGGGCATCGATCGGATGGGAGTGGGAATGCTGTATCT
ATAGCCCTCCAAATCAGAAGAGACAGGAATTCACAGGCCTCGAGTCCCAGTATTTTTATT
GAAGTCTGAAGAAACAAGTTCCAGAAAACATGTTAAACTTCTTCTGGGAGCTGGGGTTG
GGGGTCAGGGCTCAAGCCCAGCAGCTTCCACTCAGGGTCCCCATTTGCACCTCCGCAGGG
CAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACAC
CCTGGTGAGGAGAGACCCAGGGGTGGCGGGGTGAGGATGGGGCCAGCTCAGCCCCCTC
AAGCCACCGGATTTCTGCCTTCCCAGTTCTTGACTCGGCACCGAACTTGAACCACACC
AAACAGCGTCTCCTGGAAGTCGCCAACTACCTGGACCAGGTGGGGGCGGCGGGGAGAGA

FIG. 20D

GCGGTGATGGGGGTGGCGGCGGCAGGACAGGCAGGTGCTGGTGGGGTTTGGGGAAGAGGA
AGGGCGCCCCACGAAGGACCACCGGCGGATGGGGCGCCCTGTCCCGGCTTCAGCCCCGC
CTCGCCCTCAGCTTCTCAGGACTCTGGACATTAGGTGGCGCTGACCGGCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCC
TGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGT
GGGTGCCTCTGACCCGGACGCGGGTCCCGGGTGGGGCGGCCTCACCTCCCGGCCCCGCCT
GGTCACGCCGCGCTCCGCCCCAGGGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGC
GCCCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGTGAGCCCCGC
GGGCGGGGGCGAGGGAGAGACAGGAGGCTCTACGGCCGCGAGTGACCGCCCTCCACGGCC
CCCCAGGACCACTCGGAGCTCCCCATCGGCGCCGCGAGCCACCATGGCCCATGAGATCGGC
CACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGAGGCTGCGGCCGAGTCC
GGAGGCTGCGTACGTGGCTGCGGCCACCGGTACGCGGGTGGGGGTGGGGCTGGGGCTGG
GGCGGCTAGTCTGGGGACTTCCTCCGCTGCGTTCCTTTGGTTCGTCCCTCAGTTTCCTCT
TCTGTAAAATGGGGATAATGATCATAGTGTCCGCTTCAGGGTGGTTTATGAGGCTTAAAG
GGAAGAAGCTCAGGCAAAGTGGATTCTCAACGGTATGAAGATTATTTTCCGAGTAACCTG
GCGAGGTTACTCCTACACCGGGAGGAGACCGTTCGGGTGCGGATTCCACCTGGGTCCCG
GGCTGCTCACTATTGGGGCCGATCGTCCCCTGTCCCGCTTGTGTGTGACTTTGCGCGG
GTTACTTCCCCTCTCTGGGCTCTGCGCGTCTGGCGGCTGTAGCCAAGCCAGGGGTGGGG
ATCAGAGAAGCGCGGGGGTTGGGGGACTGTCCCTCCATGCCCAATGCCCTCCCCGTGCCG
GTAGGCACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCCGCCAGCTGCGCGCCTTCT
TCCGCAAGGGGGGCGGCGCTTGCCCTCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGC
CGGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCC
AGGTTAAGTCGGCTCGCCCGGCCCCACTTGCCCTCTCCGCTCAGGTCTGGGGCGCTGCG
CCCTCACCTGGGCCCTTCTTGCCCTTCTGGTCCCAGGAGTGCCGCGACCTCTGCTGCTTT
GCTCACAACCTGCTCGCTGCGCCCCGGGGGCCAGTGCGCCACGGGGACTGCTGCGTGCGC
TGCCCTGGTGAGGGCATGGAAGGTTAGGGTGAGGGTTTTCGGGGAGCTTGGGAGCCGGCCT
GTTGGCCTTAGTTAATTGGTGCCCTCAGGTTCCCCCGTTGGGTGCTGGGCTTGGGTAGGC
CTGGCTCCCCAGCTCCGAGCCGCGCTCTCGGCATGGACCTCTCACTGCACGTGGCCTCT
CTCTGCCTTCCCCACCACCCGTCACCTGCGCAGCTGAAGCCGGCTGGAGCGCTGTGCCGC
CAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTGACAGGGCACCTCCTCCCACTGTCCC
CCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCTACTGCTGGGAT
GGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGTGAGAGGACA
CGAGACCCCTTGACCCCTGCCCCCATCCTCTGGTGGGGCCAGTTTTCTACTGTGGGGAA
GATGGGCAGGGGAACTGAGGCCCGCTGAGCGCAGCCCCCTCTCCGAGCTGCCCCGAGCT
GGCCCATGCTTCTCAGGCTCCCAACCCAGCTCCCGAGGCTGTTTCCAGGTGGTGAACTC
TGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCTGCCCCTGTGC
AGGGAGGTAGGGAGTGGAGCTGAGTGGAGGGAGCAGAAGCTATGGAGTGGGTTTGGGGAA
GGGGGGTACTGCAGCTGTTGACCCCCCTCTACTTCTCCCGAGGATGCCCTGTGTGGGA
AGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACT
CTACCGTTACCTAGATGGCCAGGAAGTGACTTGTGGGGAGCCTTGGCACTCCCCAGTG
CCCAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAA
TGGTGAGCTCTGCCCACCCGACCCCTCCTTGCCGTTTGAATCCCGCAGGCCAGTGTCCCC
CTCACTGCCTGGTGCACTGCCCCGTAGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCT
TCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTGAGAGCCCAGGAG
TGGGGGTGACCTTGGGGTTCTTAATCCTACGTGACCCCTCCTTCTCTCTCTGTCAGGTT
TGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAG
CCAGGCTTTGGTGCCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAGTATGCCAGTGGGG
GGCATGTGGGCAGGAGCTGGGGTGGTGACCTGCTCAGGACTCAGCGCCCCCTTCCCCAA
TCCCCGAGACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGC
TCCAGGGGCGGGCCTGGCCTGGTGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGAT
GCAGCTGGGGCTGCAGAAGGGACCCCTGCGTGCACTGGGTAGGCTCCGAGCGCCTGCTTCC

FIG. 20E

TGAGCCTACTCCTGCGGTTCCCCTCCTCAGAGCTCTGCTGGGGCTGTGGGAGCTGGGGCA
GGCCCTCAGCCTTGCCCCCAGGTGCAGAGAGCAGCCCCAGAGGCCATGGAAAGAAGTAGC
TTTGAACAGGAGGTTCAGTGGCCTCCAGTCAAGCGAGGGGGTGGATCCCTGCCCCACC
ACCAGCACGCAAGGCATGGCCCTCTACCTCCAGTACAGCTCCTCTTGTCCACTCTCCT
GCTTCTCCCACCAGCTGGCTGCCTCACCCCTTGACTTCGCCCTGTTTTTCCCTGGCTCAGA
TTGCAGTCCCTGTACCATGCTGCCCCCGGAGGCCTGTCCAGCCTCTGTCTCACCAGTTTT
CGGCCCTTTGCCACTTCCTCTGCACAAATCACCTCTGTCACCCCCTTGAAGTTCCCAAAT
GCTGGGCCCAGCACATCTTTTCACTCCATAACCACTGGTCAGCTGCGGTGCTGGCTGCCCC
TGTGCCAGGGCCCTGCCTTAACCCAGTTCTCTGTGACCTGGGTGGTGGCGGAGTGGGGAG
TCACATAATACTAAGCATGGCTGTCTAGGACTCACCTGCACCAGGGCCCTAGGCAGGG
CAGGCACTCTGTGGCCATGTCTGACATAGCCTGGTCTTGGGAGTGTCTCCGGGCAAGCCAA
GGGAGATGGCATGATTTGGGCCAGAGATGGGGGCAGAGGGCATAACAGACAGGGGCAGGG
CACCACCTGGGCCCCGGGTGGCAGCTAAGAGGACCCTGACAAAGCGAGTTGTGATTGAGG
GTCTGTGGGCAGAGGAGCAAGGTGGCCAGAGCCTGGCGTGTGAGCAGCGAGGGGCGCTG
CAGAGGGTGGCGGCTGCTTCTCATCCCCAGGCGGGAGTCTCAGGGCAGGGGAGATGTTT
TGAAGGAACATCACAGGAAATGACAAGGCCTTGGGGGATGGGATGGGGACAGTCAAAGAT
GGCTTGAATCATCAAGGGCAGCAGGGCACCCAGGGGCAAGGAGAGCAGACATAGCTGCC
GAAGGGGCGGACATCCAAGGTTCTTTGGAAGCTGAGCGATGCCAGCATCTGGAGAGTGCC
AGGCTGCTGGGTGGTGTGAGAGCCTGGAGGAAATGTTAGGACTAGAGAGAGGAGGTGCCA
GCCGAGGGCATGAGGCTCACTTGGAGCCTGGATCCCAAGGCTCCCCTGAAGAGGGAGCAG
GAAGGGAGCTGAGAGGGTGACTTGGAGCAGATGGGTGCCCCAAGAACTCAGTAAACGCA
GAATCCCTGGGCTGGACACCATGCTGCGGGGAGGCAATAACCCACTCAGGATCACTGTG
CCAACCTCCTGGACTCTTATCACGTTGCTCAGCCCCAAAGATGGCCCCACACAGGGACCAC
CCCCCTGGGCGGCGTTCACCCCATGGAGTTGGGGCCCCACAGCCACTGGACAGCCCTGGCCC
CTGGGTGAGTGAGGCACCAGGGGGAGGTGGAGAGGGGAAGGGAGAAGGGCTCATGC
CTCCTGCCTCCTTCCAGATGGGCAGCACCCAGTCACCTTGAGTCCCCTATGCCCTCCCC
AGCCCCAGGGTCTCCTGCTGACCATATTCAACAATTTACCCTCCACCATTCTCCCAGA
CCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCC
TGACCCCCAAGGTAGGCAGGGACCTGGATTCAAAGCCTCCCCCTCTCATCGCCCACCCTC
CCACCTCTCCCACCCCTCAGTTTGCTGCCCCCTAATCAGGTTTCTGGGCTCAGGTTATTA
TGGAATGAGTTTATGACCTCTTGTTATCATGGAGACCAGGATGCTGGAAGCCCCCTGGG
CTGGGGAGGGAGAAGCTGTGGCTTTTCTGGATCACTGGTCTCACTGAGTGAGGATGGG
CTCTCTGCCACACAGCTTGAGCCTGGGGCCCGAGTCTTAGGGGACAACATATCCTCCT
CATTCTCAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTA
AAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTGCAG
GGGCAGAGCCAGTGAATCACCGGACCTCCAGCCTGCAGGCAGCTTGGAAGTTTCTTCC
CCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACACTAGAAGTTCTGAG
GGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAA
AGGTCACACAGCCCCTGACCTCCCTCACAGTGGAGGCTGGGTAGTGCTGGCCATCCCAA
AAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTC
TGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTGACTGA
GTCCCACTCCCCTGGAGCCTGGCTGGCCTCTGCAACAAACATAATTTTGGGGACCTTC
CTTCTGTCTTCTCCCACCCTGTCTTCTCCCCTAGGTGGTTCTTGAGCCCCCACCCTCAA
TCCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATTTCTGT
GTGTGTCGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGA
AAGCATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCT
GGGGTAGGAGGATCACCAGAGGCCAGGAGGTCCACACCAGCCTGGGCAACACAGCAAGAC
ACCGCATCTACAGAAAAATTTTAAATAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCT
AGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAG
CTATGGTGGCACCCTGCCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATA
AATTTTAAAAAGACATATTACACTTGGACCTTGTTAGTCTTTTCTGTATGTAAATTCAA

FIG. 20F

CCCATGGGGTGCCCTGAGGACCACACGGGGTGGTGGTTGGCGGGGTGGTGGTTGGTGGGG
TGGTGGCTGACGGGGTGGTGGCTGGCAGGCCGAGCCTAGATGGCAGCCAGAGCCCCAGGC
ATGTGTCTGGGCACAGGACGGTGTGCTTAGTTTGAACACCCTCTTTGCTCTGTCACTCC
TGCCCTCCCTTGGGCGTTTACATTCTCCCATTTGCTTCATGCAAGAGCTGCTGAGTGGCCTA
TATCAGCCAGCTGTTGCCGCATAACAAAACCATCCCAAACTGAGTGCAGGGAGGCAACT
TCACCTCGGGCTCCACTCCACAAGCCCAAGGGGCCAGGTGAGAGTGCTCTCTAAAGCCCC
CTCCTGCCCTCAGTTGTAGTTGCAAAATTTTAATTTATGAAGGTGACTGATGACACAGAGG
CCAATGCTGTTGAAATAAGTTATTACTCACAGTTTCCACCATGCAGGGCCACAGTGGGG
AGGCACTAGGTTTGGTCCAGGGACAGAATCAGGAGCGAGTGGAAGGCACAGGCCACAGCC
CACAGTGCCGTTTCCACTGGGGAGGCAAGGCAGGCCAGGGGAAGAGGGTAGGATTGGCAT
TTTGAATCATTCTGGTGGGGTTTGGGGCGTGGGGTTGGGCTCTAATTGTCTGGGTAGGTG
CCTGGCCCTGAGCTGGTTTLAGGGCAGGGGAAATACTGGTTTCGTATGTGAGAGTTCCTTG
AAGGGGGTGGTTGGTGTATGGACTCAAGACTGGTCGGTTTGCATATGAAAGGCATGAGTT
GTTTCTGATCTCCAGGAATCAAGCAGTTTCTCTCCAGCCAACAAGCCCCACCCGAGAT
GTTAAACCATCATAAAATAGAGAATCTAAGGCCAGGCATGGTGGCTCACGCCTGTAATCC
CAGCACTTTGGGAGGCCAAGGCGGGAGGATCATTGAGGTGAGAAGTTCGAGACCAGCCT
GGCCAATGTGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCCGGTGTGGTGGC
ACGTGCCTATAATCCCAGCTACTCGGGAGGCTGCGGCAGGAGAATTGTTTGAACATGGGA
GGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGCAACAAGAGCA
AGACTCCGTCTCAAAAAAAAAAAAAAAAAAAGAGAGACTCTAAAAATACACGTTAATAT
ACCTCCCCCGCTCTTACCCTTCAGGAGGGGGTGTCTAGACCCCGCGGGACTCCAGCTACA
AGGGACCCCTGGGGAGGCCAACTCTGCCCTCTTGGCTAATCCCCAAGACTGCCCAGCACCC
CCTCCACCCCTTCTCCATTCACTGGCGAACCTGGGGAGGCCACGTGGGAAGGAAAGAGG
GCTCTAAGAGGGGAGGCCCCAGACTGGGGGAGAGGCCTGTCTGGAGCCCAGGATCACCTG
GCTGTGCTGCAGAACTGGAGAAGAGAAGCTCAGCAGAAAGGAGCTGGCATGGGGCCAACA
GCAGAAAAGCAGGAGGCACGCAGAAGTGACTGGGAAGCAGGAGGGTAGGCATGGACCCTG
AGGCTGAGCAGGAGGTACTGAGGGGCAGAGTGACGCTGAGCTGGGGGTAGCGAGCGAGC
CCAGCTCAGCTGTGACGCCCTCTGTTTGGCCACCCAACTACCAGCTACTTGGGCTGCCCC
GGGAGGAACTGGGCTTCCTCTGACATTCTGTGGCCTGCGGCCATCTGTACACCTTCTTC
TCTCTCTGCCCCCTCCCTTGACTTGTGGCACCCACAGACAGGTGGGAGAGTGTACCTGCCC
TGTGTGGTCAGAGCTTGGTTTTGAGTTTCCCTTCCCTCACCCCTCTTTCCTCCACACGCC
AAAACACAAGAGGATGTGTGAGAGGCCTGTGAACCAGAGCAACTCCATCCTGAATAGGGG
CTGAGCAAAATAAGGCTGAGACCTACTGGGCTGCGTTTCCAGACAGTTACAGCATTCTGC
GTCACAGGATGAGATAGGAGATACAGGTCTAAAGACCTTGCTGATAAAATAGTTTGCAG
TAGGCCAGGCGCGGTAGCTCACGCCTGTAATCCCAGCACT

FIG. 20G